
WATER

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:16:02 1998: Maspar time 0.08 Seconds
422.695 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-7
Description: (1-125) from US08844215 pep
Perfect Score: 949
Sequence: 1 EVOLLESGSEVKKPGSSVKV

Scoring table: PAM 150
Gap 11

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: p1r53
1:ann1 2:ann2 3:ann3 4:ann4 5:ann5 6:ann6 7:ann7
8:ann8 9:ann9 10:ann10 11:ann11 12:ann12 13:ann13
14:ann14 15:ann15 16:ann16 17:ann17 18:unrev

Statistics: Mean 40.893; Variance 107.589; scale 0.380

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	754	79.5	125 7 PH0957 Ig heavy chain V reg 4.99e-96
2	671	70.7	128 7 PH0952 Ig heavy chain V reg 4.62e-83
3	661	69.7	129 7 A33548 Ig heavy chain V-1 r 1.66e-81
4	657	69.2	116 7 PH0959 Ig heavy chain V reg 6.97e-79
5	648	68.3	132 7 PH0958 Ig heavy chain V reg 1.75e-79
6	646	68.1	120 7 PH0962 Ig heavy chain V reg 3.57e-79
7	642	67.7	126 7 B33548 Ig heavy chain V-1 r 1.49e-78
8	642	67.7	127 7 PH0955 Ig heavy chain V reg 1.49e-78
9	639	67.3	132 7 PH0954 Ig heavy chain V reg 4.37e-78
10	638	67.2	119 7 PH0961 Ig heavy chain V reg 6.24e-78
11	634	66.8	121 7 A49590 Ig heavy chain V reg 2.61e-77
12	633	66.7	135 7 PH0953 Ig heavy chain V reg 3.72e-77
13	632	66.6	133 7 C33548 Ig heavy chain V-1 r 5.32e-77
14	632	66.6	627 7 S14683 Ig mu chain precursor 5.32e-77
15	629	66.3	98 7 S26915 Ig heavy chain V reg 1.55e-76
16	629	66.3	116 7 S31698 Ig heavy chain precursor 1.55e-76
17	629	66.3	123 7 S4108 Ig heavy chain V-D-J 1.55e-76
18	628	66.2	115 7 S36261 Ig heavy chain V reg 2.22e-76
19	627	66.1	198 7 S24580 Ig heavy chain V-1 r 3.17e-76
20	622	65.5	136 7 PH0960 Ig heavy chain V reg 1.89e-75

21	620	55.3	132 7 S46394 Ig heavy chain V reg 3.86e-75
22	619	55.2	119 7 S44106 Ig heavy chain V-D-J 5.51e-75
23	616	64.9	113 7 PH1663 Ig heavy chain V reg 1.61e-74
24	595	62.7	98 7 S46463 Ig heavy chain V-1 r 2.85e-74
25	592	62.4	135 7 B32274 Ig heavy chain precursor 8.28e-71
26	591	62.3	117 2 G1HUEU Ig heavy chain V-1 r 1.18e-70
27	591	62.3	122 7 B49590 Ig heavy chain V reg 1.18e-70
28	585	61.6	132 7 C49590 Ig heavy chain V reg 9.97e-70
29	584	61.5	97 7 PH0870 Ig heavy chain V reg 1.42e-69
30	581	61.2	150 7 PL0105 anti-PR2 erythrocyte 4.13e-69
31	578	60.9	116 7 S31667 Ig heavy chain V reg 1.20e-68
32	572	60.3	98 7 A20523 Ig heavy chain V-1 r 1.01e-67
33	567	59.7	108 7 PH1664 Ig heavy chain V-1 r 5.94e-67
34	567	59.7	123 7 D33548 Ig heavy chain V-1 r 5.94e-67
35	559	58.9	124 7 S19665 Ig heavy chain V reg 1.01e-65
36	557	58.7	129 7 S36260 Ig heavy chain V reg 2.05e-65
37	556	58.6	136 7 I44151 Ig heavy chain V reg 2.93e-65
38	555	58.5	109 7 PH1671 Ig heavy chain V reg 4.17e-65
39	554	58.4	171 7 S23623 Ig heavy chain V reg 5.94e-65
40	545	57.5	148 7 S23257 Ig heavy chain V reg 1.01e-63
41	545	57.4	122 7 S36271 Ig heavy chain V reg 1.43e-63
42	539	56.8	127 7 S34014 Ig heavy chain V reg 1.19e-62
43	539	56.8	142 7 A32483 Ig heavy chain V reg 1.19e-62
44	538	56.7	129 7 S46393 Ig heavy chain V reg 1.70e-62
45	536	56.5	118 7 S36265 Ig heavy chain V reg 3.45e-62

ALIGNMENTS

RESULT 1
ENTRY PH0957 #type fragment
TITLE Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
ORGANISM #normal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
ACCESSION PH0957
REFERENCE PH0952
AUTHORS Martin, I., Duffy, S.F., Barsby, B.A., Kipps, T.J.
J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MIM:2202880
#accession PH0957
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-125 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotrimer; immunoglobulin
FEATURE
1-30
15-98
31-35
36-50
51-67
68-98
99-113
SUMMARY #length 125 #checksum 8143
#region framework 1\
#domain immunoglobulin homology #label IMM\
#region complementarity-determining 1\
#region framework 2\
#region complementarity-determining 2\
#region framework 3\
#region complementarity-determining 3
#length 125 #checksum 8143

Query Match: 79.5% Score 754, DB 7, Length 125.
Best Local Similarity 83.8%; Pred No. 4.99e-96;
Matches 107; Conservative 9; Mismatches 7; Indels 5; Gaps 3;
Db 1 gvalvsgaavkpgssvkvscasgttssvaimwrrgpgggglwmgilpigtany 60
|||||
QY 1 EVOLLESGSEVKKPGSSVKVSPASGSGSFPSYFNWVRQAPGQGLEWMGSIIPMFGTANY 60
61 aqfqrvtatdestntaymelslrsdtaavyocard-g--csggscyfwgfdpwgq 117
|||||
QY 61 AQFQFQFVTTTADSTATGYMELSLPSECTAVYVCAMPYKHCGRGSC--WGWFDPWQ 118
Db 118 gtlvtvss 125
QY 119 GTLVTVSS 126


```

#journal      J. Exp. Med. (1992) 175:983-991
#title        Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession    PH0955
##status      nucleic acid sequence not shown
##molecule_type DNA
##residues    1-127 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE
1-30          #region framework 1\
15-98         #domain immunoglobulin homology #label IMM\
31-35         #region complementarity-determining 1\
36-50         #region framework 2\
51-67         #region complementarity-determining 2\
68-98         #region framework 3\
99-115        #region complementarity-determining 3
SUMMARY
length 127 #checksum 6297

Query Match      67.7%; Score 642; DB 7; Length 127;
Best Local Similarity 74.0%; Pred. No. 1.49e-78;
Matches 94; Conservative 13; Mismatches 19; Indels 1; Gaps 1;

Db 1 qvqlvsgaevkpssvkvscasggtfssyaiswvraqpgqlwmqgllpifgtany 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVQLLESGSEVKKPGSSVKVSCFASGSGFRPSYFNWVQAPQCGLEKMWGGIIPMGFTANY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 akkfgrvritadeststymelsslrdsedtavvycarvsvfvgvhyvyyndvsgk 120
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 AKKFGQGRVITADESTATGYMELSSLRSEDATAVVYCARVSKPGRSGSCWGF-DPMFGQ 119
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 121 tvtvss 127
1-111
QY 120 TLTVTSS 126

RESULT 9
ENTRY      PH0954
TITLE      Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0954
#authors    Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal    J. Exp. Med. (1992) 175:983-991
#title      Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession  PH0954
##status    nucleic acid sequence not shown
##molecule_type DNA
##residues  1-132 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE
1-30          #region framework 1\
15-98         #domain immunoglobulin homology #label IMM\
31-35         #region complementarity-determining 1\
36-50         #region framework 2\
51-67         #region complementarity-determining 2\
68-98         #region framework 3\
99-120        #region complementarity-determining 3
SUMMARY
length 132 #checksum 9232

Query Match      67.1%; Score 639; DB 7; Length 132;
Best Local Similarity 72.7%; Pred. No. 4.37e-78;
Matches 96; Conservative 16; Mismatches 14; Indels 6; Gaps 3;

Db 1 qvqlvsgaevkpssvkvscasggtfssyaiswvraqpgqlwmqgllpifgtany 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVQLLESGSEVKKPGSSVKVSCFASGSGFRPSYFNWVQAPQCGLEKMWGGIIPMGFTANY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 akkfgrvritadeststymelsslrdsedtavvycarvsvfvgvhyvyyndvsgmd 120

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||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 AAKFGQGRVITADESTATGYMELSSLRSEDATAVVYCARVSKPGRSGSCWGF-DPMFG 114
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 121 vwdqggtvtvss 132
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 115 PWGGGTLTVTSS 126

RESULT 10
ENTRY      PH0961
TITLE      Ig heavy chain V region (G6+ T-L33) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0961
#authors    Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal    J. Exp. Med. (1992) 175:983-991
#title      Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession  PH0961
##status    nucleic acid sequence not shown
##molecule_type DNA
##residues  1-119 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE
1-30          #region framework 1\
15-98         #domain immunoglobulin homology #label IMM\
31-35         #region complementarity-determining 1\
36-50         #region framework 2\
51-67         #region complementarity-determining 2\
68-98         #region framework 3\
99-107        #region complementarity-determining 3
SUMMARY
length 119 #checksum 8601

Query Match      67.2%; Score 638; DB 7; Length 119;
Best Local Similarity 85.0%; Pred. No. 6.24e-78;
Matches 85; Conservative 11; Mismatches 4; Indels 0; Gaps 0;

Db 1 qvqlvsgaevkpssvkvscasggtfssyaiswvraqpgqlwmqgllpifgtany 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVQLLESGSEVKKPGSSVKVSCFASGSGFRPSYFNWVQAPQCGLEKMWGGIIPMGFTANY 60
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db 61 akkfgrvritadeststymelsslrdsedtavvycarv 100
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 AKKFGQGRVITADESTATGYMELSSLRSEDATAVVYCARV 100
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
ENTRY      A49590
TITLE      Ig heavy chain V region (ACHSV1, clone 15) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
23-May-1997
ACCESSIONS A49590
#authors    Burioni, R.; Williamson, R.A.; Sanna, P.P.; Bloom, F.E.;
            Burton, D.R.
#journal    Proc. Natl. Acad. Sci. U S A (1994) 91:355-359
#title      Recombinant human Fab to glycoprotein B neutralizes
            infectivity and prevents cell-to-cell transmission of
            herpes simplex viruses 1 and 2 in vitro.
#cross-references MUID:94105168
#accession  A49590
##status    preliminary, not compared with conceptual translation
##molecule_type nucleic acid
##residues  1-121 ##label BUR
##cross-references NCBI:141850
##experimental_source bone marrow lymphocytes
##note      #sequence extracted from NCBI backbone
            #superfamily immunoglobulin V region; immunoglobulin homology
            heterotetramer; immunoglobulin

```



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QY 114 DPWGGTTLVTYSS 126

RESULT 15
ENTRY S26915 #type fragment
TITLE Ig heavy chain V region (DP-10) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
06-Jun-1997
ACCESSIONS S26915
REFERENCE S26885
#authors Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.;
Winter, G.
#journal J. Mol. Biol. (1992) 227:776-798
#title The repertoire of human germline V(H) sequences reveals about
fifty groups of V(H) segments with different hypervariable
loops.
#accession S26915
##status Preliminary
##molecule_type DNA
##residues 1-98 ##label TOM
##cross-references EMBL:Z12312
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY #length 98 #checksum 3310

Query Match 66.3%; Score 629; DB 7; Length 98;
Best Local Similarity 86.6%; Pred. No. 1.55e-76;
Matches 84; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Db 1 qvqlvqsgaevkpgssvkscasqgtfssyaiswvrqapggqlwmggiipifgtany 60
QY 1 EYQLLESGEVKKPGSSVKVSCFASGSGSPSYNFNVPAPGQGLEWMGGIIPMEGTANY 60
Db 61 aqkfggrvtitadeststaymelsslrsestavyyca 97
QY 61 AQKFGGRVTITADESTATGYMELSLRSEDTAVYYCA 97

Search completed: Tue Feb 24 07:16:18 1998
Job time : 16 secs.

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WQREH (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:42:43 1998; MasPar time 3.28 Seconds
195.669 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-7
Description: (1-126) from US08844215.pep
Perfect Score: 949
Sequence: 1 EVOLLESGSEVKKPGSSVKV ... GSCWGWFDPPWGGTLLVTYS 126

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2.51 3.52 4 53 5 54 6 55 7 56 8:PCR90 9 PCR1
10:PCR92 11:PCR93 12:PCR94 13:PCR95 14:PCR96

Statistics: Mean 28.440; Variance 143 456; scale 0 198

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	635	66.9	120	11	PCT-US93-1 Sequence 13, Applicati	1.04e-42
2	609	64.2	120	11	PCT-US93-1 Sequence 12, Applicati	1.48e-40
3	605	63.8	129	13	PCT-US95-0 Sequence 45, Applicati	3.18e-40
4	604	63.6	147	6	US-08-217- Sequence 4, Applicati	3.85e-40
5	595	62.7	102	10	PCT-US92-0 Sequence 55, Applicati	2.14e-39
6	595	62.7	102	7	US-08-053- Sequence 63, Applicati	2.14e-39
7	595	62.7	102	7	PCT-US92-1 Sequence 63, Applicati	2.14e-39
8	595	62.7	102	7	US-07-834- Sequence 55, Applicati	2.14e-39
9	591	62.3	117	7	US-08-474- Sequence 15, Applicati	4.58e-39
10	591	62.3	117	6	US-08-477- Sequence 104, Applicat	4.58e-39
11	591	62.3	117	6	US-08-477- Sequence 4, Applicati	4.58e-39
12	591	62.3	117	6	US-08-477- Sequence 15, Applicati	4.58e-39
13	591	62.3	117	6	US-08-477- Sequence 72, Applicati	4.58e-39
14	591	62.3	117	6	US-07-634- Sequence 15, Applicati	4.58e-39
15	591	62.3	117	6	US-07-634- Sequence 4, Applicati	4.58e-39
16	591	62.3	117	6	US-07-634- Sequence 72, Applicati	4.58e-39
17	591	62.3	117	6	US-07-634- Sequence 104, Applicat	4.58e-39
18	591	62.3	117	7	US-08-474- Sequence 4, Applicati	4.58e-39
19	591	62.3	117	7	US-08-487- Sequence 15, Applicati	4.58e-39
20	591	62.3	117	7	US-08-487- Sequence 72, Applicati	4.58e-39
21	591	62.3	117	7	US-08-474- Sequence 104, Applicat	4.58e-39
22	591	62.3	117	7	US-08-474- Sequence 72, Applicati	4.58e-39

23	591	62.3	117	7	US-08-487- Sequence 4, Applicatio	4.58e-39
24	591	62.3	117	7	US-08-487- Sequence 104, Applicat	4.58e-39
25	587	61.9	122	13	PCT-US95-0 Sequence 2, Applicatio	9.82e-39
26	553	58.3	98	6	US-08-211- Sequence 140, Applicat	6.31e-36
27	553	58.3	128	7	US-08-478- Sequence 63, Applicati	6.31e-36
28	545	57.4	140	11	PCT-US93-1 Sequence 12, Applicati	2.88e-35
29	540	56.9	119	13	PCT-US95-0 Sequence 12, Applicati	7.45e-35
30	536	56.5	121	11	PCT-US93-1 Sequence 8, Applicatio	1.59e-34
31	532	56.1	97	14	PCT-US96-0 Sequence 16, Applicati	3.40e-34
32	531	56.0	116	7	US-08-487- Sequence 6, Applicatio	4.11e-34
33	531	56.0	116	6	US-08-477- Sequence 6, Applicatio	4.11e-34
34	531	56.0	116	6	US-07-634- Sequence 6, Applicatio	4.11e-34
35	531	56.0	116	7	US-08-474- Sequence 6, Applicatio	4.11e-34
36	526	55.4	121	6	US-07-634- Sequence 53, Applicati	1.06e-33
37	526	55.4	121	7	US-08-487- Sequence 53, Applicati	1.06e-33
38	526	55.4	121	6	US-08-477- Sequence 53, Applicati	1.06e-33
39	526	55.4	121	7	US-08-474- Sequence 53, Applicati	1.06e-33
40	524	55.2	119	13	PCT-US95-0 Sequence 10, Applicati	1.55e-33
41	523	55.1	123	13	PCT-US95-0 Sequence 11, Applicati	1.87e-33
42	523	55.1	142	13	PCT-US95-0 Sequence 17, Applicati	1.87e-33
43	522	55.0	119	13	PCT-US95-0 Sequence 13, Applicati	2.26e-33
44	519	54.7	140	6	US-07-946- Sequence 28, Applicati	3.99e-33
45	518	54.6	97	13	PCT-US95-1 Sequence 13, Applicati	4.82e-33

ALIGNMENTS

RESULT 1
ID PCT-US93-10555-13 STANDARD: PPT: 120 AA.

XX

AC xxxxxx

DT 01-JAN-1900

DE Sequence 13, Application PC/TUS9310555.

XX Sequence 13, Application PC/TUS9310555

CC GENERAL INFORMATION

CC APPLICANT: SILVERMAN, GREGG J.

CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF

CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES

CC THROUGH

CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG

CC ATES

CC TITLE OF INVENTION: THEREOF

CC NUMBER OF SEQUENCES: 51

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Spensley Horn Jubas & Lubitz

CC STREET: 1890 Century Park East - Suite 500

CC CITY: Los Angeles

CC STATE: California

CC COUNTRY: USA

CC ZIP: 90067

CC COMPUTER READABLE FORM.

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US93/10555

CC FILING DATE: 29-OCT-1993

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Howells, Stacy L.

CC REGISTRATION NUMBER: 34,842

CC REFERENCE/DOCKET NUMBER: PD-2630

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 455-5100

CC TELEFAX: (619) 455-5110

CC INFORMATION FOR SEQ ID NO: 13:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 120 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: KAS
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..120
SQ SEQUENCE 120 AA: 13008 MW: 78865 CN:

Query Match 66 %; Score 635; DB 11; Length 120;
Best Local Similarity 73.8%; Pred. No. 1.04e-42;
Matches 93; Conservative 15; Mismatches 11; Indels 7; Gaps 6;
Db 1 VHLVQSGAEVKKPGSSVKYSCKASGTFSSYAISWVP-APGSGIFEMWGSIPIPIFQANYA 60
QY 2 VOLLEGSEVKKPGSSVKYSCKASGTFSSYFNFNWVPQAPQGLEWMGNIIIMFGSIANYA 61
Db 61 QKFGQVTTITADESTNTATMELRLSRSDTAMYYCAKESGDY-CP-P-ED-F--WQGGT 114
QY 62 QKFGQVTTITADESTATGYMELSSLPSELTAVYYCAMP-YPKH-SFGS-SWQWFGDQWPGT 120
Db 115 LVTSS 120
QY 121 LVTSS 126

RESULT 2
ID PCT-US93-10555-12 STANDARD: PRT: 120 AA.

XX XXXXXX
XX 01-JAN-1900
XX Sequence 12. Application PC/TUS93/10555
XX Sequence 12. Application PC/TUS93/10555
CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
CC THROUGH
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG

CC ATES
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: PD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 120 amino acids
CC TYPE: amino acid

CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: BOR
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..120
SQ SEQUENCE 120 AA: 12984 MW: 80846 CN:

Query Match 64 %; Score 609; DB 11; Length 120;
Best Local Similarity 72.0%; Pred. No. 1.48e-40;
Matches 90; Conservative 19; Mismatches 11; Indels 5; Gaps 2;
Db 1 VHLVQSGAEVKKPGSSVKVKTKAS-ITFSSAISWVE-APGSGIFEMWGSIPIPIFQANYA 60
QY 2 VOLLEGSEVKKPGSSVKVKTKASGTFSSYFNFNWVPQAPQGLEWMGNIIIMFGSIANYA 61
Db 61 QKFGQVTTITADESTNTATMELRLSRSDTAMYYCAKESGDY-CP-P-ED-F--WQGGT 114
QY 62 QKFGQVTTITADESTATGYMELSSLPSELTAVYYCAMP-YPKH-SFGS-SWQWFGDQWPGT 120
Db 116 VTVSS 120
QY 122 VTVSS 126

RESULT 3
ID PCT-US95-01219-45 STANDARD: PRT: 129 AA.

XX XXXXXX
XX 01-JAN-1900
XX Sequence 45. Application PC/TUS95/01219.
XX Sequence 45. Application PC/TUS95/01219
CC GENERAL INFORMATION:
CC APPLICANT: Bendig, Mary M.
CC APPLICANT: Leger, Olivier J.
CC APPLICANT: Saldanha, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against Lookocyte
CC TITLE OF INVENTION: Adhesion Molecule VLA-4
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khearie and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent in Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/01219
CC FILING DATE: 25-JAN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/196,269
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-5040
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 45:
CC SEQUENCE CHARACTERISTICS:

QY 61 AOKFOGRVITADSTATGYMELSSLRSDTAVYYCA 97

RESULT 6
ID US-08-053-131-63 STANDARD; PRT; 102 AA.

XX

AC

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XX

DT 01-JAN-1900

XX

DE

XX

Sequence 63, Application US/08053131.

XX

Sequence 63, Application US/08053131

CC

Patent No. 5661016

CC

GENERAL INFORMATION:

CC

APPLICANT: Lonberg, Nils

CC

APPLICANT: Kay, Robert M.

CC

TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for

CC

TITLE OF INVENTION: Producing Heterologous Antibodies

CC

NUMBER OF SEQUENCES: 197

CC

CORRESPONDENCE ADDRESS:

CC

ADDRESS: Townsend and Townsend Kourie and Crew

CC

STREET: One Market Plaza, Steuart Tower, Suite 200

CC

CITY: San Francisco

CC

STATE: California

CC

COUNTRY: USA

CC

ZIP: 94105

CC

COMPUTER READABLE FORM:

CC

MEDIUM TYPE: Floppy disk

CC

COMPUTER: IBM PC compatible

CC

OPERATING SYSTEM: PC-DOS/MS-DOS

CC

SOFTWARE: Patent In Release #1.0, Version #1.25

CC

CURRENT APPLICATION DATA:

CC

APPLICATION NUMBER: US/08/053,131

CC

FILING DATE: 26-APR-1993

CC

CLASSIFICATION: 800

CC

PRIOR APPLICATION DATA:

CC

APPLICATION NUMBER: US 07/990,960

CC

FILING DATE: 16-DEC-1992

CC

PRIOR APPLICATION DATA:

CC

APPLICATION NUMBER: US 07/910,279

CC

FILING DATE: 17-DEC-1991

CC

PRIOR APPLICATION DATA:

CC

APPLICATION NUMBER: US 07/853,408

CC

FILING DATE: 18-MAR-1992

CC

ATTORNEY/AGENT INFORMATION:

CC

NAME: Smith, William M.

CC

REGISTRATION NUMBER: 30,223

CC

REFERENCE/DOCKET NUMBER: 14643-9-3

CC

TELECOMMUNICATION INFORMATION:

CC

TELEPHONE: 415-326-2400

CC

TELEFAX: 415-326-2422

CC

INFORMATION FOR SEQ ID NO: 63:

CC

SEQUENCE CHARACTERISTICS:

CC

LENGTH: 102 amino acids

CC

TYPE: amino acid

CC

TOPOLOGY: linear

CC

MOLECULE TYPE: protein

CC

SEQUENCE 102 AA: 10940 MW: 55781 CN:

SQ

Query Match 62.7%; Score 595; DB 7; Length 102;
Best Local Similarity 82.5%; Pred. No. 2,14e-39;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db 5 QVOLVSGAEVKKPGSSVKVSKASGGTSSVAISWVRQAPGQGLEWMGRIPIILGIANY 64

QY 1 EVQLLESGEVRKPGSSVKVSKASGGTSSVAISWVRQAPGQGLEWMGRIPIILGIANY 60

Db 65 AOKFOGRVITADKSTSTAYMELSSLRSDTAVYYCA 101

QY 61 AOKFOGRVITADSTATGYMELSSLRSDTAVYYCA 97

RESULT 7

ID PCT-US92-10983-63 STANDARD; PRT; 102 AA.

XX

AC

XX

XX

DT 01-JAN-1900

XX

DE

XX

Sequence 63, Application PCT/US9210983.

XX

Sequence 63, Application PCT/US9210983

CC

GENERAL INFORMATION:

CC

APPLICANT: Lonberg, Nils

CC

APPLICANT: Kay, Robert M.

CC

TITLE OF INVENTION: Transgenic Non-Human Animals for

CC

TITLE OF INVENTION: Producing Heterologous Antibodies

CC

NUMBER OF SEQUENCES: 152

CC

CORRESPONDENCE ADDRESS:

CC

ADDRESSEE: William M. Smith

CC

STREET: One Market Plaza, Steuart Tower, Suite 2000

CC

CITY: San Francisco

CC

STATE: California

CC

COUNTRY: USA

CC

ZIP: 94105

CC

COMPUTER READABLE FORM:

CC

MEDIUM TYPE: Floppy disk

CC

COMPUTER: IBM PC compatible

CC

OPERATING SYSTEM: PC-DOS/MS-DOS

CC

SOFTWARE: Patent In Release #1.0, Version #1.25

CC

CURRENT APPLICATION DATA:

CC

APPLICATION NUMBER: PCT/US92/10983

CC

FILING DATE: 19921217

CC

CLASSIFICATION:

CC

ATTORNEY/AGENT INFORMATION:

CC

NAME: Smith, William M.

CC

REGISTRATION NUMBER: 30,223

CC

REFERENCE/DOCKET NUMBER: 14643-9-2

CC

TELECOMMUNICATION INFORMATION:

CC

TELEPHONE: 415-326-2400

CC

TELEFAX: 415-326-2422

CC

INFORMATION FOR SEQ ID NO: 63:

CC

SEQUENCE CHARACTERISTICS:

CC

LENGTH: 102 amino acids

CC

TYPE: AMINO ACID

CC

TOPOLOGY: linear

CC

MOLECULE TYPE: protein

CC

SEQUENCE 102 AA: 10940 MW: 55781 CN:

SQ

Query Match 62.7%; Score 595; DB 10; Length 102;
Best Local Similarity 82.5%; Pred. No. 2,14e-39;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db 5 QVOLVSGAEVKKPGSSVKVSKASGGTSSVAISWVRQAPGQGLEWMGRIPIILGIANY 64

QY 1 EVQLLESGEVRKPGSSVKVSKASGGTSSVAISWVRQAPGQGLEWMGRIPIILGIANY 60

Db 65 AOKFOGRVITADKSTSTAYMELSSLRSDTAVYYCA 101

QY 61 AOKFOGRVITADSTATGYMELSSLRSDTAVYYCA 97

RESULT 8

ID US-07-834-539A-55 STANDARD; PRT; 102 AA.

XX

AC

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XX

DT 01-JAN-1900

XX

DE

XX

Sequence 55, Application US/07834539A.

XX

Sequence 55, Application US/07834539A

CC

Patent No. 5633425

CC

GENERAL INFORMATION:

CC

APPLICANT: Lonberg, Nils

CC

CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic No. 5633425-Human Animals Capable of
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 77
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: William M. Smith
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/834,530A
CC FILING DATE: 19920205
CC CLASSIFICATION: 800
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-5
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 55:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 102 amino acids
CC TYPE: AMINO ACID
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 102 AA: 10940 MW: 55781 CN:
SQ
Query Match 62.7% Score 595; DB 7; Length 102;
Best Local Similarity 82.5% Pred No 2 14e-39;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;
Db 5 QVQLVSGAEVKKPKGSSVKVSKASGCTFSSVAISWVQAPQGLWNGRIIPILGIANY 64
QY 1 EVQLLESGSEVKKPKGSSVKVSKASGCTFSSVAISWVQAPQGLWNGRIIPILGIANY 60
Db 65 AQKFGQGVITADKSTSTAYMELSSLSRSEDATVYYCA 101
QY 61 AQKFGQGVITADESTATGYMELSSLSRSEDATVYYCA 97
RESULT 9
ID US-08-474-040-15 STANDARD: PRT: 117 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 15, Application US/08474040.
XX
Sequence 15, Application US/08474040
CC Patent No. 5693761
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELLING, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULIN
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto

CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/474,040
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 536
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 325-2400
CC TELEFAX: (415) 325-2422
CC INFORMATION FOR SEQ ID NO: 15:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..117
CC OTHER INFORMATION: /note: "Eu heavy chain amino acid
CC OTHER INFORMATION: sequence."
SQ SEQUENCE 117 AA: 12472 MW: 77871 CN.
Query Match 62.3% Score 591; DB 7; Length 117;
Best Local Similarity 79.0% Pred. No. 4.58e-39;
Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps 0.
Db 1 QVQLVSGAEVKKPKGSSVKVSKASGCTFSSVAISWVQAPQGLWNGRIIPILGIANY 60
QY 1 EVQLLESGSEVKKPKGSSVKVSKASGCTFSSVAISWVQAPQGLWNGRIIPILGIANY 60
Db 61 AQKFGQGVITADESTNTAYMELSSLSRSEDATVYFCAGY 100
QY 61 AQKFGQGVITADESTATGYMELSSLSRSEDATVYYCAMPY 100
RESULT 10
ID US-08-477-728-104 STANDARD: PRT: 117 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 104, Application US/08477728.
XX
Sequence 104, Application US/08477728
CC Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.

CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend and Crew LLP
 CC STREET: Two Embarcadero Center, 8th Floor
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94111
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/477,728
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/634,278
 CC FILING DATE: 19-DEC-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002600
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 104:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 117 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 62.3%; Score 591; DB 6; Length 117;
 Best Local Similarity 79.0%; Pred. No. 4,58e-39;
 Matches 79; Conservative 11; Mismatches 10; Indels 0; Caps 0;
 Db 1 QVQLVQSGAEVKKPGSSVKVSCKASGGSFSSRSALIIWVRQAPGQGLEWMGGIVPMFGFPNY 60
 QY 1 EVQLLESGSEVKKPGSSVKVSCKASGGSFSSRSYFNWVRQAPGQGLEWMGGIIPMFGTANY 60

Db 61 AOKFOGRVTITADESTNTAYMELSSLRSEDTAFYFCAGGY 100
 QY 61 AOKFOGRVTITADESTATGYMELSSLRSEDTAVYYCAMPY 100

RESULT 11
 ID US-08-477-728-4 STANDARD: PRT: 117 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900

XX Sequence 4, Application US/08477728.
 XX Sequence 4, Application US/08477728
 CC Patent No. 5585089
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: SCHNEIDER, William P.

CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend and Crew LLP
 CC STREET: Two Embarcadero Center, 8th Floor
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94111
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/477,728
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/634,278
 CC FILING DATE: 19-DEC-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/590,274
 CC FILING DATE: 28-SEP-1990
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/310,252
 CC FILING DATE: 13-FEB-1989
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/290,975
 CC FILING DATE: 28-DEC-1988
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 11823-002600
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 4:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 117 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: unknown
 CC MOLECULE TYPE: protein
 CC HYPOTHETICAL: NO
 CC FEATURE:
 CC NAME/KEY: Protein
 CC LOCATION: 1..117
 CC OTHER INFORMATION: /note= "Variable region of the human
 CC OTHER INFORMATION: E_h antibody heavy chain."
 CC SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 62.3%; Score 591; DB 6; Length 117;
 Best Local Similarity 79.0%; Pred. No. 4,58e-39;
 Matches 79; Conservative 11; Mismatches 10; Indels 0; Caps 0;

Db 1 QVQLVQSGAEVKKPGSSVKVSCKASGGSFSSRSALIIWVRQAPGQGLEWMGGIVPMFGFPNY 60
 QY 1 EVQLLESGSEVKKPGSSVKVSCKASGGSFSSRSYFNWVRQAPGQGLEWMGGIIPMFGTANY 60

Db 61 AOKFOGRVTITADESTNTAYMELSSLRSEDTAFYFCAGGY 100
 QY 61 AOKFOGRVTITADESTATGYMELSSLRSEDTAVYYCAMPY 100

RESULT 12
 ID US-08-477-728-15 STANDARD: PRT: 117 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900
 XX

DE Sequence 15, Application US/08477728.
XX Sequence 15, Application US/08477728.
CC Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 15:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHEICAL: NO
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1..117
CC OTHER INFORMATION: /note= "Eu heavy chain amino acid
CC OTHER INFORMATION: sequence."
SQ SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 62.3%; Score 591; DB 6; Length 117;
Best Local Similarity 79.0%; Pred No 4 58e-39;
Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
Db 1 QVVLVSGAEVKKPGSSVKVSKASGTSFSAIIVWRQAPGGGLEWGGIVPMFGPPNY 60
QY 1 EVQLLESGEVEKPKGSSVKVSKASGTSFSAIIVWRQAPGGGLEWGGIVPMFGPPNY 60
Db 61 AQKFGQGVTTITADSTNTAYMELSSLSRSEDATFYFCAGGY 100
QY 61 AQKFGQGVTTITADSTNTAYMELSSLSRSEDATFYFCAGGY 100

RESULT 13
ID US-08-477-728-72 STANDARD: PPT: 117 AA.
XX AC xxxxxx
XX 01-JAN-1900
XX Sequence 72, Application US/08477728.
XX Sequence 72, Application US/08477728.
CC Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, 8th Floor
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 72:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 62.3%; Score 591; DB 6; Length 117;
Best Local Similarity 79.0%; Pred No 4 58e-39;
Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Db 1 QVVLVSGAEVKKPGSSVKVSKASGTSFSAIIVWRQAPGGGLEWGGIVPMFGPPNY 60
QY 1 EVQLLESGEVEKPKGSSVKVSKASGTSFSAIIVWRQAPGGGLEWGGIVPMFGPPNY 60
Db 61 AQKFGQGVTTITADSTNTAYMELSSLSRSEDATFYFCAGGY 100
QY 61 AQKFGQGVTTITADSTNTAYMELSSLSRSEDATFYFCAGGY 100

SQ SEQUENCE 117 AA: 12472 MW: 77871 CN;
 Query Match 62.3%; Score 591; DB 6; Length 117;
 Best Local Similarity 79.0%; Pred. No. 4.58e-39;
 Matches 79; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
 Db 1 QVQLVQSGAEVKKPGSSVKVCKASGGTFSRSATIIWVFPQAPGQGLEWMGGIVPMFGPPNY 60
 QY 1 EVQLLESGSEVKKPGSSVKVCKRSGGSGFSRSYFNWVRQAPGQGLEWMGGIIPMGFTANY 60
 Db 61 AOKFOGRVTITADESTNTAYMELSSLRSEDTAFYFCAGY 100
 QY 61 AOKFOGRVTITADESTATGYMELSSLRSEDTAVYYCAMPY 100

Search completed: Tue Feb 24 07:42:57 1998
 Job time : 14 secs.



WIREH

(TV)

Release 2 ID John F Collins, Biocomputing Research Unit,
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:16:36 1998, MasPar time 10.72 Seconds
Tabular output not generated
Title: >US-08-844-215-7
Description: (1-126) from US08844215 pep
Perfect Score: 949
Sequence: 1 EVQLLESGSEVKKPGSSVKV.GSGWGWFDPWGQGLTVTS 126

Scoring table: PAM 150
Gap 11
Searched: 111726 seqs, 13289129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-genes30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23
Statistics: Mean 30.601; Variance 151.366; scale 0.202

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				%		Query		Match Length DB		ID		Description		Pred. No.	
Result	No.	Score	Match	Length	DB	ID									
1	773	81.5	481	5	R24442							Sequence of antibody		2.26e-54	
2	678	71.4	476	6	R31023							Antibody D heavy chain		2.54e-45	
3	635	66.9	120	9	P54796							SpA-reactive IgM heavy		1.07e-42	
4	634	66.8	123	23	W19887							CEA-specific antibody		1.30e-42	
5	629	66.3	98	12	R72068							DP10 VH region.		3.43e-42	
6	621	65.4	123	23	W19898							CEA-specific antibody		1.62e-41	
7	620	65.2	123	23	W19886							CEA-specific antibody		1.97e-41	
8	618	65.1	122	23	W19880							CEA-specific antibody		2.90e-41	
9	617	65.0	123	23	W19891							CEA-specific antibody		3.55e-41	
10	604	63.6	147	12	P65019							gA9 anti-Varicella		4.36e-40	
11	603	63.5	249	14	P77610							Humanised 5G1.1 VH +		5.30e-40	
12	598	63.0	119	23	W13536							Anti-melanoma antibod		1.39e-39	
13	595	62.7	98	12	P72069							HV1263 VH region		2.49e-39	
14	595	62.7	117	7	R38233							Human heavy chain V r		2.49e-39	
15	595	62.7	117	4	R23358							Protein encoded by th		2.49e-39	
16	595	62.7	117	20	W03950							DNA fragment wh49.8		2.49e-39	
17	592	62.4	249	14	R77615							Humanised 5G1.1 VH +		4.45e-39	
18	591	62.3	117	2	R24104							Human antibody Eu hea		5.40e-39	
19	591	62.3	118	5	R28742							Heavy chain variable		5.40e-39	
20	587	61.9	122	14	P76964							HSV-neutralising anti		1.17e-38	

21	586	61.7	102	5	P25325							Hv region of human rh		1.42e-38	
22	585	61.6	248	14	R77416							Humanised CDP-grafted		1.72e-38	
23	581	61.2	120	9	P54795							SPA-reactive IgM heavy		3.74e-38	
24	580	61.1	124	9	P45610							Monoclonal antibody G		4.53e-38	
25	566	59.6	248	14	R77607							Humanised CDR-grafted		6.78e-37	
26	566	59.6	249	14	R77611							Humanised 5G1.1 VH +		6.78e-37	
27	563	59.3	142	9	P50188							Heavy chain variable		1.21e-36	
28	559	58.9	222	7	R39267							Humanised C4G1 Ig hea		2.62e-36	
29	559	58.9	235	7	R39268							Humanised C4G1 Ig hea		2.62e-36	
30	554	58.9	449	7	P43339							Completely humanised		1.23e-35	
31	551	58.1	142	9	P50194							Heavy chain variable		1.23e-35	
32	547	57.6	468	5	P28828							pre-5A8 humanised hea		2.65e-35	
33	545	57.4	121	14	R77874							Humanised mouse DRG-2		3.90e-35	
34	545	57.4	149	9	P55556							DRG-200 Humanized an		4.72e-35	
35	544	57.3	145	22	W22341							Human anti-tumour ant		1.72e-35	
36	543	57.2	98	12	P72070							OFH1.2 VH-1 H chain.		5.73e-35	
37	540	56.9	119	15	R81324							Humanized VLA-4 antib		1.02e-34	
38	540	56.9	119	23	W22425							Humanized alpha-4 int		1.02e-34	
39	539	56.9	125	9	P45609							Monoclonal antibody G		1.24e-34	
40	536	56.5	98	6	R34372							Mutated human VH1 gen		2.31e-34	
41	535	56.4	139	11	R62679							CV1748RHB VH region.		2.67e-34	
42	535	56.4	142	9	P50186							Heavy chain variable		2.67e-34	
43	534	56.3	118	10	R60305							Chimeric anti HIV ant		3.24e-34	
44	534	56.3	140	23	W21847							Humanised heavy chain		3.24e-34	
45	534	56.3	142	9	P50193							Heavy chain variable		3.24e-34	

ALIGNMENTS

RESULT 1
ID R24442 standard: Protein; 481 AA.
AC R24442;
DE 02-JAN-1992 (first entry)
DT Sequence of antibody molecule IgG1.
KW Antibody; immunoglobulin G1.
OS Homo sapiens.
PH Key Location/Qualifiers
FT Misc-difference 308
FT /label= N
FT /note= "Substn. to create glycan addition site"
FT Misc-difference 310
FT /label= S
FT /note= "see above"
FT Misc-difference 321
FT /label= N
FT /note= "see above"
FT Misc-difference 329
FT /label= N
FT /note= "see above"
FT Misc-difference 331
FT /label= S
FT /note= "see above"
FT Misc-difference 356
FT /label= N
FT /note= "see above"
FT Misc-difference 369
FT /label= N
FT /note= "see above"
FT Misc-difference 379
FT /label= N
FT /note= "see above"
FT Misc-difference 393-A.
FT W0329293-A.
FT 11-JUN-1992.
FT 18-NOV-1991; US8605.
FT 23-NOV-1990; US-518314.
FT (GENO) GEN HOSPITAL CORP.
FT Seed B, Waltz G;
FT WPI: 92-215789/26.
FT N:PSDB: Q25443.
FT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
FT - used in treating chronic inflammation, rheumatoid arthritis,
FT psoriasis, etc.
FT Disclosures; Fig 1; 46pp; English.
FT The IgG1, in its nascent form, bears no sialyl-Lex side chains. The
FT inventors designed a molecule including several such sites for
FT attachment of sialyl-Lex side chains (see P24442, FI). The

CC additional N-linked glycosylation sites are introduced at locations
CC which impair complement fixing and Fc receptor binding ability. They
CC are preferably located in the C_{H2} region of the Ig molecule.
CC Antibodies bearing multiple sialyl-Lex determinants are useful for
CC disrupting undesirable interactions between cells or proteins.
CC Disrupting this interaction has therapeutic applications, for
CC example, in minimising inflammation following tissue injury.
SQ Sequence 481 AA:

Query Match 81.5% Score 773; DB 5; Length 481;
Best Local Similarity 82.7% Pred No. 2 26e-54;
Matches 105; Conservative 11; Mismatches 10; Indels 1; Gaps 1;

Db 25 qvqlvsgaevkpgssvskvscasggtfssyalswvrgapqgglwmgdliplfgtany 84
QY 1 EVQLLESGSEVKKPGSSVKVSCPASGSPFSYFNFNVRGAPQGI FWMGSIIPMFGIANY 60
Db 85 aqkfgqrvtitadestaymelstsrdsdtauyycardngaycsgsgscyswfdpwqgs 144
QY 61 AQKFGQRTVITADESTATGYMELLSURSEDVAVYYCAMPYPKHCSGSGSCW-GWFDPWQGS 119
Db 145 tlvtvss 151
QY 120 TLVTVSS 126

RESULT 2
ID R31023 standard; Protein: 476 AA.

AC R31023;
DE Antibody D heavy chain.
KW Heavy; light; chain; antibody; D. monoclonal; peripheral; blood;
KW lymphocyte; hepatitis A virus; HAV; sero; positive; patient;
KW murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.
OS Synthetic.

Location/Qualifiers

FT Key
FT Peptide 1..19
FT /note= "Signal peptide"
FT /region 20..49
FT /label= FR1
FT /region 50..54
FT /label= CDR1
FT /region 55..68
FT /label= FR2
FT /region 69..84
FT /label= CDR2
FT /region 85..113
FT /label= FR3
FT /region 114..121
FT /label= CDR3
FT /region 122..132
FT /label= FR4
FT /domain 133..241
FT /label= CH1
FT /region 242..262
FT /label= HINGE
FT /domain 263..379
FT /label= CH2
FT /domain 380..497
FT /label= CH3
PN EP-523949-A.
PD 20-JAN-1993.
PE 14-JUL-1992; 306420.
PR 15-JUL-1991; GB-015284.
PR 01-AUG-1991; GB-016594.
PR 23-MAP-1992; GB-006284.
PA (WELL) WELLCOME FOUND. LTD.
PI Crowe JS, Lewis AP;
DR WPI: 93-019551/03.
DR N-P5DB: Q35099.

PT Prodn. of recombinant primate antibodies - useful for treating
PT infections caused by hepatitis A, B and C, herpes
PT cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,

PT arthritis etc.
PS Disclosure; Fig 2: 35pp; English.
CC The sequences given in Fig 2: 24 represent the heavy and light chains
CC of Antibody D respectively. Antibody D is a monoclonal antibody which
CC was derived from peripheral blood lymphocytes from a hepatitis A virus
CC (HAV) sero positive patient. Antibody D is closely related in nature
CC to murine antibody B5B3. Total RNA was isolated from antibody D
CC expressing cells and polyadenylated RNA was extracted. These polyA
CC RNA's were used to prepare a cDNA library which was screened for human
CC kappa light (L) chains and two positive clones were detected.
CC Further heavy (H) chain clones were also isolated.
SQ Sequence 476 AA:

Query Match 71.4% Score 678; DB 6; Length 476;
Best Local Similarity 71.1% Pred. No. 2 52e-46;
Matches 91; Conservative 20; Mismatches 14; Indels 3; Gaps 3;

Db 20 qmrvvsgaevkpgssvskvscasggtfssyalswvrgapqgglwmgdliplfgtany 79
QY 1 EVQLLESGSEVKKPGSSVKVSCPASGSPFSYFNFNVRGAPQGI FWMGSIIPMFGIANY 60
Db 80 sqnfgqrvtitadestaymelstsrdsdtauyycardngaycsgsgscyswfdpwqgs 148
QY 61 AQKFGQRTVITADESTATGYMELLSURSEDVAVYYCAMPYPKHCSGSGSCW-GWFDPWQGS 118
Db 139 gtlvtvss 146
QY 119 GTLVTVSS 126

RESULT 3

ID R54796 standard; peptide, 120 AA.

AC R54796;
DE SPA-reactive IgM heavy chain clone KAS.
KW SPA domain D; Ig binding region; IgM; B-cell superantigen; SAQ;
KW superantigen; heavy chain variable region; VH3 restricted antibody;
KW VH; protein-A; KAS; B-lymphocyte; vaccine.
OS Homo sapiens.
PN WO9409818-A.
PD 11-MAY-1994.
PF 29-OCT-1993; U10555.
PR 30-OCT-1992; US-966936.
PA (REGC) UNIV CALIFORNIA.
PI Silverman GJ;
DR WPI: 94-167127/20.
PT Stimulating prodn. of variable region gene family restricted
PT antibodies - through B cell super-antigen vaccination
PS Disclosure; Page 78; 130pp; English.
CC A B-cell superantigen (SAQ) is a fragment of SPA D domain that
CC specifically binds the Fab portion of variable region of VH, especially
CC antibodies. The SAQ is used to enhance production of VH, especially
CC VH3, restricted Abs. During attempts to identify SAQs, aa sequences
CC (R54784-801) of H chains from Ig reactive with mod-SPA, and aa and
CC ENA sequences (R54802-15, 04842-5) of VH regions of SPA binders
CC obtained from combinatorial libraries were determined. IgM protein
CC KAS is derived from the germline configuration of a VH gene
CC segment.
SQ Sequence 120 AA:

Query Match 66.9% Score 635; DB 9; Length 120;
Best Local Similarity 73.8% Pred. No. 1 07e-42;
Matches 93; Conservative 15; Mismatches 11; Indels 7; Gaps 6;

Db 1 vhlvsgaevkpgssvskvscasggtfssyalswvrgapqgglwmgdliplfgtany 60
QY 2 VQLLESGSEVKKPGSSVKVSCPASGSPFSYFNFNVRGAPQGI FWMGSIIPMFGIANY 61
Db 61 qkfgqrvtitadestaymelstsrdsdtauyycardngaycsgsgscyswfdpwqgs 114
QY 62 QAKFGQRTVITADESTATGYMELLSURSEDVAVYYCAMPYPKHCSGSGSCW-GWFDPWQGS 120
Db 115 lvtvss 120

|||||
QY 121 LVTSS 126

RESULT 4
ID W19887 standard; Protein: 123 AA.
AC W19887;
DE CEA-specific antibody CEA6 VH mutant HBAl1 sequence.
KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
KW tumour marker; lung cancer; breast cancer; colon cancer;
KW adenocarcinoma; diagnosis.
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..66
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 99..112
FT /label= CDR3
FT /note= "complementarity determining region 3"
PN WO9720932-A1.
PD 12-JUN-1997.
PF 09-DEC-1996; G03043
PP 11-OCT-1996; GR-021295.
PP 07-DEC-1995; GR-025004.
PR 23-MAY-1996; GR-010824.
PR (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Allen DJ, McCafferty JG, Osbourn JK;
DR WPI: 97-319779/29

PT Specific binding members for human carcinoembryonic antigen - bind to the A3-B3 extracellular domain of hCEA and are substantially non-cross-reactive with human liver cells; used for diagnosing PT cancer.
PS Claim 4; Fig 2; 128pp: English.
CC This polypeptide sequence comprises the heavy chain variable region (VH), HBAl1, obtained by mutagenesis of the VH CDR3 of human carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see W19881). A claimed specific binding member (A) comprises an hCEA specific antibody antigen binding domain that has a dissociation constant for hCEA of less than 1 x 10⁻⁸ M, is non-cross-reactive with human liver cells, and preferentially binds to the A3-B3 extracellular domain of hCEA and/or to cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis or chain shuffling. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast. Sequence 123 AA;

Query Match 66.8%; Score 634; DB 23; Length 123;
Best Local Similarity 73.0%; Pred. No. 1,306-42;
Matches 92; Conservative 19; Mismatches 12; Indels 3; Gaps 3;

Db 1 qvalvsgaevkpgssvskvscasggtfssvlsvalsvrrqapqgglewmgslpifgtany 60
QY 1 EVQLLESGSEVKKPGSSVSKVSPASGGSFPFYNFNVVPQAPGSGLEWMGSLPMPFTANY 60
Db 61 aqfqrlltadeatstaymelslrsedtavyyca-g-anoncrsvyy-ymdvrgggt 117
QY 61 AQKQFQGRVITADESTATGYMELSLRSED TAVYYCAMYPKPKHCSPGSCWGWDFDVGQGI 120

Db 118 mvtvss 123
QY 121 LVTSS 126

RESULT 5
ID R72068 standard; Protein: 98 AA.

AC R72068;
DT 26-SEP-1995 (first entry)
DE DP10 VH region.
KW Graves ophthalmopathy associated immunoglobulin protein; orbital antigen; monoclonal antibody; heavy chain; H chain; variable region; autoimmunity.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50..66
FT /label= CDR2
PN WO9508336-A.
PD 30-MAR-1995.
PF 22-SEP-1994; U10756.
PF 22-SEP-1993; US-124469.
DR (NICH-) NICHOLS INST DIAGNOSTICS.
PI McLachlan SM, Rapoport B;
DR WPI: 95-139383/18.
DR N-PSDB; Q89327.
PT Graves' ophthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCR.
PS Disclosure: Page 68; 94pp: English.
CC L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (IgG1) genes showed homology to the closest germline genes, Dp10 (089327) and hL1263 (289328). The DNA (289329) and corresp. amino acid (R72070) sequences of the VH region of a representative clone, CC 2F7H1.2, are provided.
SQ Sequence 98 AA;

Query Match 66.3%; Score 629; DB 12; Length 98;
Best Local Similarity 86.6%; Pred. No. 3,436-42;

Matches 84; Conservative 11; Mismatches 2; Indels 0; Gaps 0;

Db 1 qvalvsgaevkpgssvskvscasggtfssvlsvalsvrrqapqgglewmgslpifgtany 60
QY 1 EVQLLESGSEVKKPGSSVSKVSPASGGSFPFYNFNVVPQAPGSGLEWMGSLPMPFTANY 60
Db 61 aqfqrlltadeatstaymelslrsedtavyyca 97
QY 61 AQKQFQGRVITADESTATGYMELSLRSED TAVYYCA 97

RESULT 6
ID W19888 standard; Protein: 123 AA.

AC W19888;
DT 07-DEC-1997 (first entry)
DE CEA-specific antibody CEA6 VH mutant HBB11 sequence.
KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
KW tumour marker; lung cancer; breast cancer; colon cancer;
KW adenocarcinoma; diagnosis.
OS Chimeric Homo sapiens;
OS Chimeric synthetic.

FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..66
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 99..112
FT /label= CDR3
FT /note= "complementarity determining region 3"
PN WO9720932-A1.
PD 12-JUN-1997.

PF 09-DEC-1996; G03043.
PP 11-OCT-1996; GR-021295.
PP 07-DEC-1995; GR-025004.
PR 23-MAY-1996; GR-010824.
PR (CAME-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Allen DJ, McCafferty JG, Osbourn JK;

DR WPI: 97-319779/29.
 PT Specific binding members for human carcinoembryonic antigen - bind
 PT to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells; used for diagnosing
 PT cancer
 PS Claim 4: Fig 2: 128pp: English.
 CC This polypeptide sequence comprises the heavy chain variable region
 CC (VH), HBB11, obtained by mutagenesis of the VH CDR3 of human
 CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19881). A claimed specific binding member (A) comprises an hCEA
 CC specific antibody antigen binding domain that has a dissociation
 CC constant for hCEA of less than 1 x 10⁻⁸ M, is non-cross-reactive
 CC with human liver cells and preferentially binds to the A3-B3
 CC extracellular domain of hCEA and/or to cell-associated hCEA over
 CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
 CC VL sequences from CEA1-7 (see W19876-85), or their CDR sequences,
 CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
 CC mutagenesis or chain shuffling. An example of a claimed pairing
 CC is HBB11 VH with CEA6 VL. (A) is used to detect cells expressing
 CC hCEA, in vivo or in vitro, especially tumour cells for diagnosing
 CC cancer, e.g. adenocarcinoma of the colon, lung or breast.
 SQ Sequence 123 AA;

Query Match 65.4%; Score 621; DB 23; Length 123;
 Best Local Similarity 73.0%; Pred. NO. 1.62e-41;
 Matches 92; Conservative 16; Mismatches 15; Indels 3; Gaps 3;
 Db 1 qvqlvsgaevkpgssvkscasggtfnsplnrlrqpqgqlwmgsllpsftany 60
 QY 1 EVQLLESGSEVKKPGSSVKVSCASGGSFSPSYNFNWRQAPGQGLWMGSIIPMFGTANY 60
 Db 61 aqkfggrltitadeststymelsslrdsedtavvyca-h-nh-nyelyyyyymdvwqggt 117
 QY 61 AQKFGGRVTITADESTATGYMELSLRSEDITAVYCYAMPYPKHCSRCWCWGFDPWQGGT 120
 Db 118 mvtvss 123
 QY 121 LVTVSS 126

RESULT 7
 ID W19886 standard; Protein; 123 AA.
 AC W19886;
 DT 07-DEC-1997 (first entry)
 DE CEA-specific antibody CEA6 VH mutant TO6D10 sequence.
 KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
 KW tumour marker; lung cancer; breast cancer; colon cancer;
 KW adenocarcinoma; diagnosis.
 OS Chimeric Homo sapiens;
 FH Chimeric synthetic.
 FT Key Location/Qualifiers
 FT Region 31...35
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 50...56
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 99...112
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FN W09720932-A1.
 PD 12-JUN-1997.
 PF 09-DEC-1996; G03043.
 PR 11-OCT-1996; GB-021295.
 PR 07-DEC-1995; GB-025004.
 PR 23-MAY-1996; GB-010824.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Allen DJ, McCafferty JG, Osbourn JK;
 DR WPI: 97-319779/29.
 PT Specific binding members for human carcinoembryonic antigen - bind
 PT to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells; used for diagnosing
 PT cancer

PS Claim 4: Fig 2: 128pp: English.
 CC This polypeptide sequence comprises the heavy chain variable region
 CC (VH), TO6D10, obtained by mutagenesis of the VH CDR3 of human
 CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19881). A claimed specific binding member (A) comprises an hCEA
 CC specific antibody antigen binding domain that has a dissociation
 CC constant for hCEA of less than 1 x 10⁻⁸ M, is non-cross-reactive
 CC with human liver cells, and preferentially binds to the A3-B3
 CC extracellular domain of hCEA and/or to cell-associated hCEA over
 CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
 CC VL sequences from CEA1-7 (see W19876-85), or their CDR sequences,
 CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
 CC mutagenesis or chain shuffling. Examples of claimed pairings are
 CC TO6D10 VH with TO6D12 or CEA6 VL. (A) is used to detect cells
 CC expressing hCEA, in vivo or in vitro, especially tumour cells for
 CC diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.
 SQ Sequence 123 AA;

Query Match 55.3%; Score 620; DB 23; Length 123;
 Best Local Similarity 72.2%; Pred. NO. 1.97e-41;
 Matches 91; Conservative 16; Mismatches 16; Indels 4; Gaps 3;
 Db 1 qvqlvsgaevkpgssvkscasggtfnsplnrlrqpqgqlwmgsllpsftany 60
 QY 1 EVQLLESGSEVKKPGSSVKVSCASGGSFSPSYNFNWRQAPGQGLWMGSIIPMFGTANY 60
 Db 61 aqkfggrltitadeststymelsslrdsedtavvyca-qcsnhyel-yyy-ymdvwqggt 117
 QY 61 AQKFGGRVTITADESTATGYMELSLRSEDITAVYCYAMPYPKHCSRCWCWGFDPWQGGT 120
 Db 118 mvtvss 123
 QY 121 LVTVSS 126

RESULT 8
 ID W19889 standard; Protein; 123 AA.
 AC W19889;
 DT 07-DEC-1997 (first entry)
 DE CEA-specific antibody CEA6 VH mutant HBB6 sequence.
 KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
 KW tumour marker; lung cancer; breast cancer; colon cancer;
 KW adenocarcinoma; diagnosis.
 OS Chimeric Homo sapiens;
 FH Chimeric synthetic.
 FT Key Location/Qualifiers
 FT Region 31...35
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 50...66
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 99...112
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FN W09720932-A1.
 PD 12-JUN-1997.
 PF 09-DEC-1996; G03043.
 PR 11-OCT-1996; GB-021295.
 PR 07-DEC-1995; GB-025004.
 PR 23-MAY-1996; GB-010824.
 PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Allen DJ, McCafferty JG, Osbourn JK;
 DR WPI: 97-319779/29.
 PT Specific binding members for human carcinoembryonic antigen - bind
 PT to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells; used for diagnosing
 PT cancer
 PS Claim 4: Fig 2: 128pp: English.
 CC This polypeptide sequence comprises the heavy chain variable region
 CC (VH), HBB6, obtained by mutagenesis of the VH CDR3 of human
 CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19881). A claimed specific binding member (A) comprises an hCEA


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DR  WEI: 95-139383/18.
DR  N-PSDB: Q89328.
PT  Graves' ophthalmopathy-associated monoclonal antibody - produced
PT  by molecular cloning of immunoglobulin genes by PCR
PS  Disclosure: Page 69; 94pp; English.
CC  L- and H-chain DNA was amplified by PCR from Graves' orbital
CC  tissue and clones encoding autoimmunity-associated immunoglobulin
CC  fragments were obtained. 13/15 clones of H chain (IgG1) genes
CC  showed homology to the closest germline genes, DP10 (Q89327) and
CC  hV1263 (Q89328). The DNA (Q89329) and correspond. amino acid
CC  (hV2070) sequences of the VH region of a representative clone,
CC  Q87H1.2, are provided.
SQ  Sequence 98 AA;

Query Match      62.7%; Score 595; DB 12; Length 98;
Best Local Similarity 82.5%; Pred. No. 2.49e-30;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db  1 qvqlvsgaevkpgssvkvsckasgtfssvaysvrrqapqggglewmgriipilgiany 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  1 EVQLLESGSEVKKPGSSVKVSCFASGSGSFPSYFNFWVFCAPGCGLEWNGSIIPMFSTANY 60

Db  61 aqkfgrrvtitadktsststymelsslrdsedtavyyca 97
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  61 AQKFGRRVTITADESTATGYMELSSLRSEDTAVYYCA 97

RESULT 14
ID  R38623 standard; Protein: 117 AA.
AC  R38623;
DE  10-NOV-1993 (first entry)
DE  Human heavy chain V region VH49.8.
KW  Immunoglobulin; IgG; heavy chain; minilocus transgene;
KW  isotype switching; H chain variable region.
OS  Homo sapiens.
PN  W09312227-A.
PD  24-JUN-1993.
PF  17-DEC-1992; U10983.
PR  17-DEC-1991; US-810279.
PR  18-MAR-1992; US-853408.
PR  23-JUN-1992; US-904068.
PA  (GENP-) GENPHARM INT INC.
PI  Kay RM, Lonberg N.
PI  WPI; 93-214169/26.
DR  N-PSDB: Q44185.
PT  Transgenic non-human animals contg. immunoglobulin heavy chain
PT  trans gene - used to produce useful antibodies by isotype
PT  switching
PS  Example 12; Page 96; 196pp; English.
CC  A human placental genomic DNA library cloned into the phage vector
CC  lambda FIX II was screened with the human VH1 family specific
CC  oligonucleotide Q44184. Phage clone lambda 49.8 was isolated and a
CC  6.1kb XbaI fragment containing the variable segment VH49.8 was
CC  subcloned into pNN03 to generate plasmid pVH49.8. An 800bp
CC  region of this insert was sequenced (Q44185) and VH49.8 found to
CC  have an open reading frame and intact splicing and recombination
CC  signals, indicating that the gene is functional. Amino acid
CC  sequence Q44185 was deduced from the coding sequence; the last 3
CC  codons before the termination codon have not been translated.
SQ  Sequence 117 AA;

Query Match      62.7%; Score 595; DB 7; Length 117;
Best Local Similarity 82.5%; Pred. No. 2.49e-39;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db  20 qvqlvsgaevkpgssvkvsckasgtfssvaysvrrqapqggglewmgriipilgiany 79
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  1 EVQLLESGSEVKKPGSSVKVSCFASGSGSFPSYFNFWVFCAPGCGLEWNGSIIPMFSTANY 60

Db  80 aqkfgrrvtitadktsststymelsslrdsedtavyyca 116
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  61 AQKFGRRVTITADESTATGYMELSSLRSEDTAVYYCA 97

Search completed. Tue Feb 24 07:16:50 1998
Job time : 14 secs.

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RESULT 15
ID  R22358 standard; Protein: 117 AA.
AC  R22358;
DE  17-AUG-1992 (first entry)
DE  Protein encoded by the human heavy chain V region gene VH49.8.
KW  Heavy chain; variable region; VH1 family.
OS  Homo sapiens.
PN  W09203918-A.
PD  19-MAR-1992.
PF  28-AUG-1991; U06185.
PR  29-AUG-1990; US-574748.
PR  31-AUG-1990; US-575962.
PA  (GENP-) GENPHARM INT INC.
PI  Lonberg N, Kay R,
PI  WPI; 92-113362/14.
DR  N-PSDB: Q22419.
PT  Immunoglobulin transgenes - for prodn. of heterologous
PT  non-rearranged and/or rearranged Ig chains
PS  Example 14; Page 87; 172pp; English.
CC  The human placental genomic DNA library cloned into the phage
CC  vector lambda FIX II was screened with the human VH1 family
CC  specific oligonucleotide (see Q22418). Phage clone lambda
CC  49.8 was isolated and a 6.1 kb XbaI fragment contg. the variable
CC  segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8.
CC  An 800 bp region of this insert was sequenced. VH49.8 was found
CC  to have an open reading frame which encoded the sequence shown..
SQ  Sequence 117 AA;

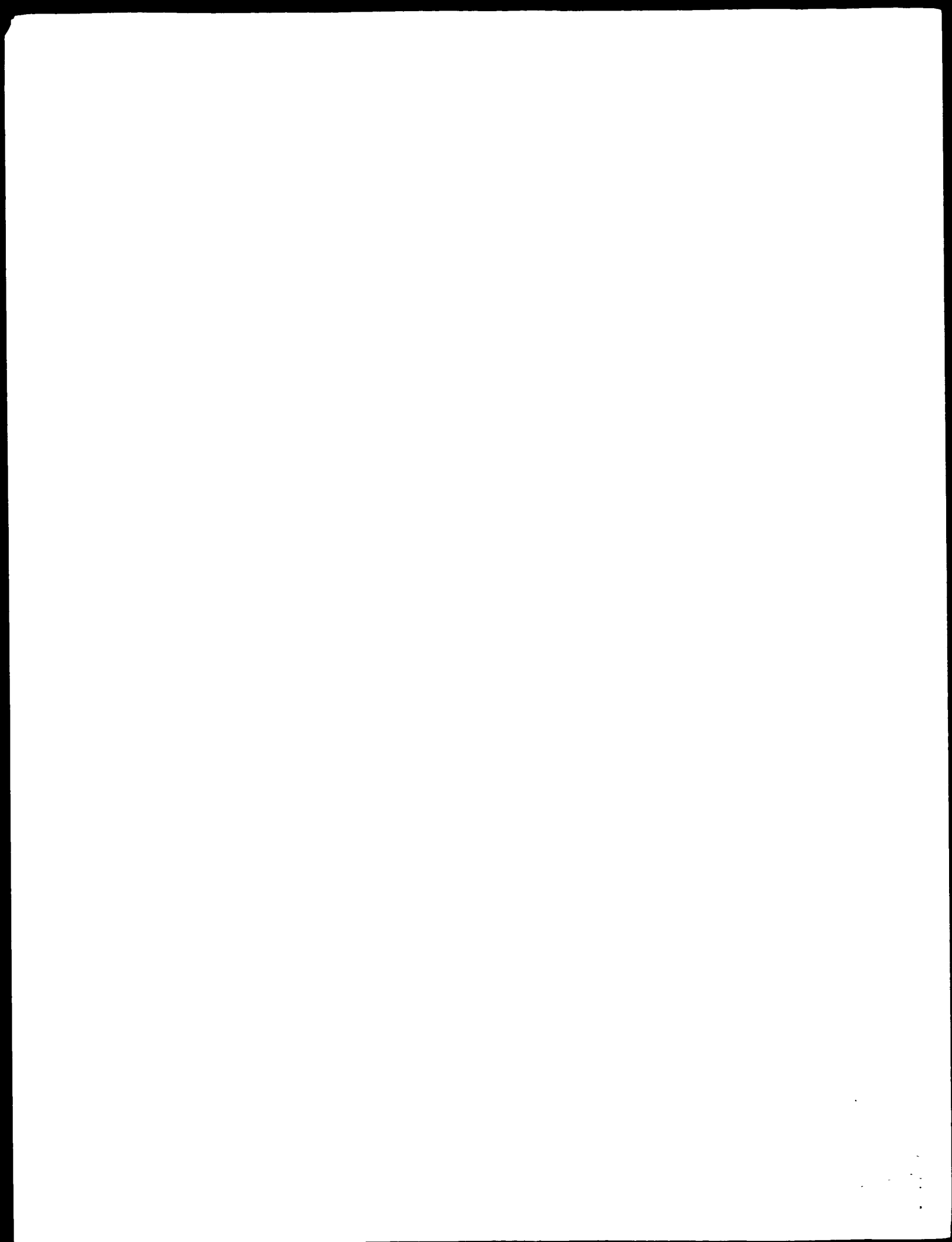
Query Match      62.7%; Score 595; DB 4; Length 117;
Best Local Similarity 82.5%; Pred. No. 2.49e-30;
Matches 80; Conservative 12; Mismatches 5; Indels 0; Gaps 0;

Db  20 qvqlvsgaevkpgssvkvsckasgtfssvaysvrrqapqggglewmgriipilgiany 79
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  1 EVQLLESGSEVKKPGSSVKVSCFASGSGSFPSYFNFWVFCAPGCGLEWNGSIIPMFSTANY 60

Db  80 aqkfgrrvtitadktsststymelsslrdsedtavyyca 116
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY  61 AQKFGRRVTITADESTATGYMELSSLRSEDTAVYYCA 97

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Search completed. Tue Feb 24 07:16:50 1998
Job time : 14 secs.




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DATE          22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
ACCESSIONS    16-Aug-1996
REFERENCE      S31690
#authors      Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.;
              Tonnelie, C.
#submission   submitted to the EMBL Data Library, June 1992
#description   Mechanisms that generate human immunoglobulin diversity
              operate from the 8th week of gestation in fetal liver.
#accession    S31690
#status       preliminary
#molecule_type mRNA
#residues     1-130 #label CUI
#cross-references EMBL:Z14199
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        20-102
SUMMARY        #domain immunoglobulin homology #label IMM
              #length 130 #checksum 491

Query Match      66.1%; Score 611; DB 7; Length 130;
Best Local Similarity 73.2%; Pred. No. 9,32e-68;
Matches 93; Conservative 12; Mismatches 19; Indels 3; Gaps 3,

Db 6 qvqlqesgplvksptslctvsggsi-svyywswsqgpkglwlgviyysgstny 64
QY 1 EVQLLESGPLVKPSGTLSTLCIVSGSIRSSHWWSVWVRQPPKGLWIGVEFFSGSTIY 60
      :||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 npslksrvtsvdknskqfslkssvtaadtavvycaarsvllwfgel-lyyfdwggg 123
QY 61 NPSLNDRVFMVSDKSDQVSLRSSVTAADTAVVYCAR-SPIKMNQGRWMLDAFDIWGGQ 119
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 tlvtvss 130
QY 120 TLVIVSS 126

RESULT 3
ENTRY      S54906 #type fragment
TITLE      IgG1 heavy chain V region - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       08-Jul-1995 #sequence_revision 03-Aug-1995 #text_change
ACCESSIONS S54906
REFERENCE   S54906
#authors    Eposito, G.; Traboni, C.
#submission submitted to the EMBL Data Library, November 1994
#description Cloning and sequencing of cDNA coding for the variable
              domains of a human antibody against Hepatitis C virus
              helicase.
#accession  S54906
#status      preliminary
#molecule_type mRNA
#residues    1-134 #label ESP
#cross-references EMBL:X82935
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
SUMMARY       #length 134 #checksum 1180

Query Match      65.7%; Score 608; DB 7; Length 134;
Best Local Similarity 71.4%; Pred. No. 2,51e-67;
Matches 90; Conservative 12; Mismatches 23; Indels 1; Gaps 1;

Db 1 qvqlqesgplvksptslctvsggsinfnwnwvrtgtpqkglwlgviyysgstny 60
QY 1 EVQLLESGPLVKPSGTLSTLCIVSGSIRSSHWWSVWVRQPPKGLWIGVEFFSGSTIY 60
      :||| ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 npslksrvtslkskflsnissvtaadtavvycaarg-lcsgsgscytgyfdkwqggt 119
QY 61 NPSLNDRVFMVSDKSDQVSLRSSVTAADTAVVYCAR-SPIKMNQGRWMLDAFDIWGGQ 120
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 120 tlvtvss 125
QY 121 LVIVSS 126

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RESULT 4
ENTRY      S26905 #type fragment
TITLE      Ig heavy chain V region (DP-70) - human (fragment)
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
ACCESSIONS S26905
REFERENCE   S26905
#authors    Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.R.;
              Winter, G.
#journal     J. Mol. Biol. (1992) 227:776-798
#title       The repertoire of human germline V(H) sequences reveals about
              fifty groups of V(H) segments with different hypervariable
              loops.
#accession  S26905
#status      preliminary
#molecule_type DNA
#residues    1-98 #label TOM
#cross-references EMBL:Z12370
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        15-98
SUMMARY        #domain immunoglobulin homology #label IMM
              #length 98 #checksum 5975

Query Match      64.6%; Score 598; DB 7; Length 98;
Best Local Similarity 83.7%; Pred. No. 6,75e-66;
Matches 82; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Db 1 qvqlqesgplvksptslctvsggsissnswswvrrppkglwlgviyysgstny 60
QY 1 EVQLLESGPLVKPSGTLSTLCIVSGSIRSSHWWSVWVRQPPKGLWIGVEFFSGSTIY 60
      :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 npslksrvtsvdknskqfslkssvtaadtavvyccar 98
QY 61 NPSLNDRVFMVSDKSDQVSLRLSSVTAADTAVVYCAR 98
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
ENTRY      S12419 #type complete
TITLE      Ig heavy chain V region (4.19) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change
ACCESSIONS S12419
REFERENCE   S09421
#authors    Sanz, I.; Kelly, P.; Williams, C.; Scholl, S.; Tucker, P.;
              Capra, J.D.
#journal     EMBO J. (1989) 8:3741-3748
#title       The smaller human V(H) gene families display remarkably
              little polymorphism.
#cross-references MUID:90059975
#accession  S12419
#status      preliminary; translation not shown
#molecule_type DNA
#residues    1-98 #label SAN
#cross-references EMBL:X56363
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        15-98
SUMMARY        #domain immunoglobulin homology #label IMM
              #length 98 #molecular_weight 10538 #checksum 5975

Query Match      64.6%; Score 598; DB 7; Length 98;
Best Local Similarity 83.7%; Pred. No. 6,75e-66;
Matches 82; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Db 1 qvqlqesgplvksptslctvsggsissnswswvrrppkglwlgviyysgstny 60
QY 1 EVQLLESGPLVKPSGTLSTLCIVSGSIRSSHWWSVWVRQPPKGLWIGVEFFSGSTIY 60
      :||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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#status      preliminary
#molecule_type  mRNA
#residues    1-155 ##label CHA
#cross-references EMBL:X69860
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE
47-129      #domain immunoglobulin homology #label IMM
SUMMARY      #length 155 #molecular_weight 1735 #checksum 9637

Query Match      62.1%; Score 574; DB 7; Length 155;
Best Local Similarity 66.7%; Pred. No. 1.80e-62;
Matches 84; Conservative 20; Mismatches 19; Indels 3; Gaps 3;

Db 33 qvqlqespglvkpseltictvsggsi-syyvswirgppkglewgiyytgsaty 91
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGPGLVKPSGTLSTCTVSGGSISSHHWSWVPPGPKGLEWIGEVEFFSGSTIY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 92 npplksrvltisvdknqfslkssvtaadtavvycaarg-gis-swydyymgmdvwgqgt 149
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 NPSLNDRVFVMSVDKQDQVSLRLSSVTAADTAVVYCAPSPIKYNQGRMLDAFDIWGQGT 120
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 150 tvtvss 155
      :|||:
QY 121 LVIVSS 126

RESULT 14
ENTRY      S31511      #type complete
TITLE      Ig heavy chain - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
          16-Aug-1996

ACCESSIONS S31511
REFERENCE   S31509
#authors    Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
#submission submitted to the EMBL Data Library, December 1992
#description Dominance of clonotypic patterns and variable gene usage of
          anti-DNA autoantibodies from patient with lupus.
#accession  S31511
#status     preliminary
#molecule_type  mRNA
#residues    1-155 ##label CHA
#cross-references EMBL:X69866
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE
47-129      #domain immunoglobulin homology #label IMM
SUMMARY      #length 155 #molecular_weight 17251 #checksum 9639

Query Match      62.1%; Score 574; DB 7; Length 155;
Best Local Similarity 66.7%; Pred. No. 1.80e-62;
Matches 84; Conservative 20; Mismatches 19; Indels 3; Gaps 3;

Db 33 qvqlqespglvkpseltictvsggsi-syyvswirgppkglewgiyytgsaty 91
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVQLLESGPGLVKPSGTLSTCTVSGGSISSHHWSWVPPGPKGLEWIGEVEFFSGSTIY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 92 npplksrvltisvdknqfslkssvtaadtavvycaarg-gis-swydyymgmdvwgqgt 149
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 NPSLNDRVFVMSVDKQDQVSLRLSSVTAADTAVVYCAPSPIKYNQGRMLDAFDIWGQGT 120
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 150 tvtvss 155
      :|||:
QY 121 LVIVSS 126

RESULT 15
ENTRY      S09710      #type complete
TITLE      Ig heavy chain V region - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
          16-Aug-1996

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ACCESSIONS S09710
REFERENCE   S09710
#authors    Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.
#journal    Biochem. J. (1990) 268:135-140
#title      Nucleotide sequences and three-dimensional modelling of the
          VH and VL domains of two human monoclonal antibodies
          specific for the D antigen of the human Rh-blood-group
          system.
#cross-references M310:90249-35
#accession  S09710
#status     preliminary
#molecule_type  mRNA
#residues    1-146 ##label HUG
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE
34-118      #domain immunoglobulin homology #label IMM
SUMMARY      #length 146 #molecular_weight 16049 #checksum 2658

Query Match      61.5%; Score 569; DB 7; Length 146;
Best Local Similarity 64.6%; Pred. No. 9.31e-62;
Matches 82; Conservative 18; Mismatches 26; Indels 1; Gaps 1;

Db 20 qlrqespglvkpseltictvsggsi-syyvswirgppkglewgiyytgsaty 79
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVQLLESGPGLVKPSGTLSTCTVSGGSISS-HWSWVPPGPKGLEWIGEVEFFSGSTI 59
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 80 ynpslksrvltisvdtlknfslkssvtaadtavvyctprpygdtsvkrvwmndlwqg 139
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 60 YNPSLNDRVFVMSVDKQDQVSLRLSSVTAADTAVVYCAPSPIKYNQGRMLDAFDIWGQGT 119
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 140 tvtvss 146
      :|||:
QY 120 TLIVSS 126

Search completed: Tue Feb 24 07:14:17 1998
Job time : 21 secs.

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100

OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE; 85205332.
 RA KUDO A., ISHIMURA T., NISHIMURA Y., WATANABE T.;
 RL GENE 33:181-189(1985).
 DR PIR: A02101; GIH02.
 DR HSP: P01825; IFGV.
 KW IMMUNOGLOBULIN V REGION; SIGNAL.

FT SIGNAL 1 19
 FT CHAIN 20 146 IG HEAVY CHAIN V-II REGION (ARR-77).
 FT DOMAIN 20 117 V SEGMENT.
 FT DOMAIN 118 127 D SEGMENT.
 FT DOMAIN 128 146 J SEGMENT.
 FT DISULFID 42 115 BY SIMILARITY.
 FT NON_TER 146 146
 SQ SEQUENCE 146 AA; 16228 MW; 72FICBA8 CRC32.

Query Match 55.48; Score 512; DB 5; Length 146;
 Best Local Similarity 60.68; Pred. No. 2.40e-87;
 Matches 77; Conservative 20; Mismatches 28; Indels 2; Gaps 2.

Db 21 qvqlqwgaglvkpsqetlsitcavfsgsf-sgyvswirgppqrglewqeiinhsgstny 79
 QY 1 EVQLLESGPGLVKPSTLSITCTVSGSIRSSHHWSWVRQPPCKGLEWIGEVFFSGSTIY 60
 Db 80 ktslksrvtlslstsknlfalkissvtaadtavvyccargllrgwvndvyygmddwggg 139
 QY 61 NPSLNDRVFMSVDKSDQVSLRSSVTAADTAVVYCARSPKMN-QGRMMLDAFDIWWGG 119
 Db 140 tvtvtvss 146
 QY 120 TLTVSS 126

RESULT 3
 ID HV2G-HUMAN STANDARD; PRT: 117 AA.
 AC P01825;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-II REGION (NEW).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]

RP SEQUENCE.
 RX MEDLINE; 77242302.
 RA POLJAK R.J., NAKASHIMA Y., CHEN B.L., KONIGSBERG W.;
 RL BIOCHEMISTRY 16:3412-3420(1977).
 RN [2]

RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF FAB FRAGMENT.
 RX MEDLINE; 78066916.
 RA SAUL F.A., AMZEL I.M., POLJAK P.J.;
 RL J. BIOL. CHEM. 253:585-597(1978).
 CC 1- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
 DR PIR: A02100; GIH0M.
 DR PDB: 7PAB; 31-JAN-94.
 KW IMMUNOGLOBULIN V REGION; 3D-STRUCTURE.
 FT MOD_RES 1 1
 FT NON_TER 117 117
 FT STRAND 3 7
 FT STRAND 11 12
 FT TURN 14 15
 FT STRAND 18 25
 FT TURN 30 31
 FT STRAND 33 39
 FT TURN 41 42
 FT STRAND 46 51
 FT TURN 53 54
 FT STRAND 57 59

FT HELIX 61 63
 FT TURN 64 66
 FT STRAND 67 72
 FT TURN 73 76
 FT STRAND 77 82
 FT HELIX 87 89
 FT STRAND 91 98
 FT STRAND 104 107
 FT STRAND 111 115
 SQ SEQUENCE 117 AA; 12790 MW; C5721B7B CRC32;

Query Match 50.98; Score 471; DB 5; Length 117;
 Best Local Similarity 66.38; Pred. No. 4.03e-78;
 Matches 67; Conservative 15; Mismatches 18; Indels 1; Gaps 1.

Db 1 qvqlqsgpqlvrpsqetlsitctvsgstf-sndyvtwrgppqrglewqeiinhsgstny 59
 QY 1 EVQLLESGPGLVKPSTLSITCTVSGSIRSSHHWSWVRQPPCKGLEWIGEVFFSGSTIY 60
 Db 60 tplsrsrvtlmldtskqfslrlssvtaadtavvyccarnli 100
 QY 61 NPSLNDRVFMSVDKSDQVSLRSSVTAADTAVVYCARSP 101

RESULT 4
 ID HV60-MOUSE STANDARD; PRT: 116 AA.
 AC P18531;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (M315).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/CJ;
 RX MEDLINE; 89279149.
 RA LEVY N.S., MALPIERO U.V., LEBERQUE S.G., GEARHART P.J.;
 RL J. EXP. MED 169:2007-2019(1989).
 DR PIR: J0509; HWS31.
 DR HSP: P01825; IBAF.

KW IMMUNOGLOBULIN V REGION; SIGNAL.
 FT SIGNAL 1 18
 FT CHAIN 19 116 IG HEAVY CHAIN V REGION (M315).
 FT DOMAIN 19 48 FRAMEWORK 1.
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 54 67 FRAMEWORK 2.
 FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 85 116 FRAMEWORK 3.
 FT DISULFID 40 114 BY SIMILARITY.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 13095 MW; 810F3E97 CRC32;

Query Match 47.68; Score 440; DB 5; Length 116;
 Best Local Similarity 59.28; Pred. No. 3.39e-71;
 Matches 58; Conservative 20; Mismatches 20; Indels 0; Gaps 0.

Db 19 dvqlqsgpqlvrpsqetlsitctvsgstfsgyvvwvwrqfqnklewqeiinhsgstny 78
 QY 1 EVQLLESGPGLVKPSTLSITCTVSGSIRSSHHWSWVRQPPCKGLEWIGEVFFSGSTIY 60
 Db 79 npslksrvtlmldtskqfslrlssvtaadtavvyccarnli 116
 QY 61 NPSLNDRVFMSVDKSDQVSLRSSVTAADTAVVYCAR 98

RESULT 5
 ID HV61-MOUSE STANDARD; PRT: 116 AA.
 AC P18532;
 DT 01-NOV-1990 (REL. 16, CREATED)
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)

DE IG HEAVY CHAIN PRECURSOR V REGION (1843)
 OS MUS MUSCULUS (MOUSE)
 OC EUKARYOTA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: RODENTIA.
 RN [1]
 PP SEQUENCE FROM N A
 RC STRAIN-BALB/CJ.
 RX MEDLINE: 89279149.
 RA LEVY N.S., MALIPIERO U.V., IERECQUE S.G., GRAHART P.J.:
 RL J. EXP. MED. 169:2007-2019(1989).
 CC -1- THIS SEQUENCE BELONGS TO THE VH3660 SUBFAMILY.
 DR HIR: JT0508: HVM51B.
 DR HSSP: P01825: 1BAF.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 18
 FT CHAIN 19 116 IG HEAVY CHAIN V REGION (1843)
 FT DOMAIN 19 48 FRAMEWORK 1.
 FT DOMAIN 49 53 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 54 67 FRAMEWORK 2
 FT DOMAIN 68 84 COMPLEMENTARITY-DETERMINING 2
 FT DOMAIN 85 116 FRAMEWORK 3.
 FT DISULFID 40 114 BY SIMILARITY
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 13158 MW; 10E4EB67 CRC32;
 Query Match 46.6%; Score 431; DB 5; Length 116;
 Best Local Similarity 60.2%; Pred. No. 3.41e-69;
 Matches 59; Conservative 18; Mismatches 21; Indels 0; Gaps 0;
 Db 19 dvalqesgdpvkpsqslsttvtgysltsgyswhirfpgnklemgmyihsgntsy 78
 QY 1 EVOLLESGPOLKPSGTLSTLCTVSGSIPSSSHWWSVPPKPKGLWIGVFFSGSTIY 60
 Db 79 npslksritskdnqfflqlnsvttedatyycar 116
 QY 61 NPSLDRVPMVDKSKDQSLSSVTAADTAVYYCAR 98
 RESULT 6
 ID HV2H HUMAN STANDARD: PRT: 147 AA.
 AC P04438.
 DT 13-AUG-1987 (REL. 05, CREATED)
 DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
 DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V-II REGION (SPSS).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: PRIMATES.
 RN [1]
 PP SEQUENCE FROM N.A.
 RX MEDLINE: 84298107.
 RA TAKAHASHI N., NOMA T., HONJO T.:
 RL PROC. NATL. ACAD. SCI. U.S.A. 81:5194-5198(1984)
 DR HIR: A02090: G2HUCS.
 DR HSSP: P01772: LGGB.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 147 IG HEAVY CHAIN V-II REGION (SPSS)
 FT DOMAIN 20 118 V SEGMENT.
 FT DOMAIN 119 132 D SEGMENT.
 FT DOMAIN 133 147 J SEGMENT
 FT NON_TER 147 147
 SQ SEQUENCE 147 AA; 16323 MW; 0994FF54 CRC32;
 Query Match 45.3%; Score 419; DB 5; Length 147;
 Best Local Similarity 49.2%; Pred. No. 1.57e-66;
 Matches 60; Conservative 26; Mismatches 34; Indels 2; Gaps 2;
 Db 20 qvnresgpalvkathltltctfslsvntgrmsvswirppgkalewlaridwdddky 79
 QY 1 EVCLLESGPLVLPSPSTLSTLCTVSGSIPSSSHWWSVPPKPKGLWIGVFFSGSTIY 59
 Db 80 yatsletritskdnqgvllkvtdmddatyyccarmqmtmrcvymitsnafdmgq 139
 Query Match 45.1%; Score 417; DB 5; Length 137;
 Best Local Similarity 58.8%; Pred. No. 4.34e-66;
 Matches 57; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

QY 60 YNPSLDRVPMVDKSKDQSLSSVTAADTAVYYCARSPKMNQSRML-DAEDINQ 118
 Db 140 gt 141
 QY 119 GT 120
 RESULT 7
 ID HV45-MOUSE STANDARD: PRT: 137 AA.
 AC P01822;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 01-AUG-1992 (REL. 23, LAST SEQUENCE UPDATE)
 DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (MOPC 315).
 OS MUS MUSCULUS (MOUSE)
 OC EUKARYOTA: METAZOA: CHORDATA: VERTEBRATA: TETRAPODA: MAMMALIA:
 OC EUTHERIA: RODENTIA.
 RN [1]
 PP SEQUENCE FROM N.A.
 RX MEDLINE: 89238351.
 RA PINFRET A., HORNE C., DORRINGTON K.J., KLEIN M.:
 RL MOL. IMMUNOL. 26:431-434(1989).
 RN [2]
 PP SEQUENCE OF 1-31.
 RX MEDLINE: 78094475.
 RA JILKA R.L., PESTKA S.:
 RL PROC. NATL. ACAD. SCI. U.S.A. 74:5692-5696(1977).
 RN [3]
 PP SEQUENCE OF 1-21.
 RX MEDLINE: 79148758.
 RA SCHRECHTER I., WOLF C., ZEMER P., BOPSTEIN Y.:
 RL FEED PROC. 38:1839-1845(1979).
 RN [4]
 PP SEQUENCE OF 19-136
 RX MEDLINE: 74170779.
 RA FRANCIS S.H., LESLIE P.G., HOOD L., EISEN H.N.:
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:1123-1127(1974).
 RN [5]
 PP REVISION TO 53.
 RX MEDLINE: 77244979.
 RA HOOD L., MAGGOLIES M.N., GIVOL D., ZAKUT P.:
 RL UNPUBLISHED RESULTS, CITED BY:
 PL PADLAN E.A., DAVIES D.P., PECHT I., GIVOL D., WRIGHT C.:
 PL COLD SPRING HARB. SYM. QUANT. BIOL. 41:627-637(1977).
 CC -1- THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN THAT HAS ANTI-DINITROPHENYL ACTIVITY.
 DR EMBL: M27638: G602707: -.
 DR EMBL: X07880: G295908: -.
 DR PIR: P0102: AYMS35.
 DR HSSP: P01789: 2FGW.
 KW IMMUNOGLOBULIN V REGION: SIGNAL.
 FT SIGNAL 1 18
 FT CHAIN 19 137 IG HEAVY CHAIN V REGION (MOPC 315).
 FT DOMAIN 19 48 FRAMEWORK 1.
 FT DOMAIN 49 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2
 FT DOMAIN 85 116 FRAMEWORK 3.
 FT DOMAIN 117 126 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 127 137 FRAMEWORK 4.
 FT DISULFID 40 114 BY SIMILARITY.
 FT CONFLICT 15 15 G -> GG (IN G295908).
 FT CONFLICT 15 15 G -> H (IN REF. 2).
 FT CONFLICT 77 78 GV -> YG (IN REF. 4).
 FT CONFLICT 102 102 N -> D (IN REF. 4).
 FT CONFLICT 123 123 MISSING (IN REF. 4).
 FT NON_TER 137 137
 SQ SEQUENCE 137 AA; 15399 MW; 155A5E8D CRC32;
 Query Match 45.1%; Score 417; DB 5; Length 137;
 Best Local Similarity 58.8%; Pred. No. 4.34e-66;
 Matches 57; Conservative 19; Mismatches 21; Indels 0; Gaps 0;

[illegible]

US-08-844-215-6.rsp

Thu Feb 26 07:06:14 1998

QY 1 EVQLLESGPGLVLPKPSGTLSTCTVSGGSIRSSHHWSWVRQPPCKGLEWIGEVFFSGSTI- 59

Db 60 ytpslkdkiisrdnaknslylqmskvrdsedtalyycar 98

QY 60 YNPSLNDRVFMVDKSKDOVSLRLSSVTAADTAAYYCARS 98

RESULT 15

ID HV41_MOUSE STANDARD; PRT; 117 AA.

AC P01811;

DT 21-JUL-1986 (REL. 01, CREATED)

DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)

DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)

DE IG HEAVY CHAIN V REGION (UPC10).

OS MUS MUSCULUS (MOUSE).

OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;

OC EUTHERIA; RODENTIA.

RN [1]

RP SEQUENCE FROM N.A.

RA AUFFRAY C., SIKORAV J.L., OLLO R., POUGEON F.;

RL ANN. INST. PASTEUR IMMUNOL 132D:77-88(1981).

CC -!- THIS CHAIN WAS ISOLATED FROM AN IG GAMMA-2A MYELOMA PROTEIN

CC BINDING 2,6-LEVAN.

DR EMBL; M36631; G194860; -.

DR PIR; A02081; G2MSU1.

DR HSP; P01810; 1FVW.

KW IMMUNOGLOBULIN V REGION.

FT NON_TER 117 117

SQ SEQUENCE 117 AA; 13001 MW; F02DB51B CRC32;

Query Match

Best Local Similarity 41.7%; Score 386; DB 5; Length 117;

Matches 54; Conservative 23; Mismatches 21; Indels 2; Gaps 2;

Db 1 evkllesgglyvpqgsklscasgfdi-sqymmswvrqpgkglewigeinpdssstin 59

QY 1 EVOLLESGPGLVLPKPSGTLSTCTVSGGSIRSSHHWSWVRQPPCKGLEWIGEVFFSGSTI- 59

Db 60 ytpflkdkiisrdnakntlfqlmskvrdsedtalyyfcar 99

QY 60 YNPSLNDRVFMVDKSKDOVSLRLSSVTAADTAAYYCARS 99

Search completed: Tue Feb 24 07:13:38 1998

Job time : 16 secs.

WIPEH

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:41:10 1998; Maspar time 3.35 Seconds
Tabular output not generated. 191.725 Million cell updates/sec

Title: >US-08-844-215-6
Description: (1-126) from US08844215.pep
Perfect Score: 925
Sequence: 1 EVQLLESGPGLVKPSGTLTL RMMLDAFDWGGTIVIVSS 126

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:PCT90 9:PCT91
10:PCT92 11:PCT93 12:PCT94 13:PCT95 14:PCT96

Statistics: Mean 28.331; Variance 154.255; scale 0.184

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	559	60.4	98	US-08-478-	Sequence 75, Applicati	1.31e-33
2	553	59.8	126	PCT-US95-0	Sequence 142, Applicat	3.78e-33
3	553	59.8	126	US-08-276-	Sequence 142, Applicat	3.78e-33
4	533	57.6	125	US-08-478-	Sequence 76, Applicati	1.28e-31
5	523	56.2	121	US-08-478-	Sequence 80, Applicati	1.25e-30
6	509	55.0	139	US-08-478-	Sequence 108, Applicat	8.66e-30
7	506	54.7	121	US-08-275-	Sequence 13, Applicati	1.47e-29
8	502	54.3	120	US-08-111-	Sequence 28, Applicati	2.96e-29
9	502	54.3	120	PCT-US93-0	Sequence 28, Applicati	2.96e-29
10	502	54.3	120	US-08-211-	Sequence 28, Applicati	2.96e-29
11	500	54.1	119	PCT-US93-1	Sequence 16, Applicati	4.20e-29
12	478	51.7	124	US-08-478-	Sequence 78, Applicati	1.98e-27
13	473	51.1	119	US-08-478-	Sequence 77, Applicati	4.75e-27
14	471	50.9	134	US-08-469-	Sequence 5, Applicatio	6.74e-27
15	471	50.9	134	US-08-259-	Sequence 6, Applicatio	6.74e-27
16	470	50.8	116	US-08-478-	Sequence 79, Applicati	8.02e-27
17	464	50.2	119	PCT-US95-1	Sequence 62, Applicati	2.29e-26
18	462	49.9	107	US-07-942-	Sequence 20, Applicati	3.25e-26
19	459	49.6	119	US-08-467-	Sequence 52, Applicati	5.48e-26
20	459	49.6	119	US-08-470-	Sequence 53, Applicati	5.48e-26
21	445	48.1	129	PCT-US93-1	Sequence 15, Applicati	6.31e-25
22	437	47.2	114	US-08-211-	Sequence 23, Applicati	2.54e-24

23	437	47.2	114	11	PCT-US93-0	Sequence 23, Applicati	2.54e-24
24	437	47.2	114	6	US-08-111-	Sequence 23, Applicati	2.54e-24
25	420	45.4	147	5	US-08-468-	Sequence 8, Applicatio	4.90e-23
26	420	45.4	147	5	US-08-259-	Sequence 9, Applicatio	4.90e-23
27	419	45.3	119	7	US-08-207-	Sequence 18, Applicati	5.82e-23
28	415	44.9	120	11	PCT-US93-1	Sequence 18, Applicati	1.77e-22
29	412	44.5	125	11	PCT-US93-1	Sequence 1, Applicatio	1.96e-22
30	411	44.4	134	10	PCT-US92-0	Sequence 15, Applicati	2.34e-22
31	411	44.4	134	7	US-08-211-	Sequence 16, Applicati	2.34e-22
32	411	44.4	134	6	PCT-US93-0	Sequence 16, Applicati	2.34e-22
33	411	44.4	134	11	US-08-111-	Sequence 19, Applicati	2.78e-22
34	410	44.3	119	7	US-08-207-	Sequence 19, Applicati	2.78e-22
35	410	44.3	124	5	US-07-958-	Sequence 4, Applicatio	2.78e-22
36	410	44.3	124	11	PCT-US93-0	Sequence 4, Applicatio	2.78e-22
37	409	44.2	119	13	PCT-US95-1	Sequence 15, Applicati	3.31e-22
38	408	44.1	119	7	US-08-459-	Sequence 12, Applicati	3.94e-22
39	404	43.7	104	7	US-07-942-	Sequence 16, Applicati	7.87e-22
40	404	43.7	121	7	US-08-275-	Sequence 9, Applicatio	7.87e-22
41	404	43.7	121	11	PCT-US93-0	Sequence 20, Applicati	7.87e-22
42	404	43.7	121	7	US-08-211-	Sequence 20, Applicati	7.87e-22
43	404	43.7	121	6	US-08-111-	Sequence 20, Applicati	7.87e-22
44	404	43.7	124	11	PCT-US93-1	Sequence 44, Applicati	7.87e-22
45	403	43.6	130	7	US-08-478-	Sequence 66, Applicati	9.36e-22

ALIGNMENTS

RESULT 1
ID US-08-478-039-75 STANDARD: PRT: 98 AA.

XX

AC xxxxxx

DT 01-JAN-1900

DE Sequence 75, Application US/08478039.

XX

CC Sequence 75, Application US/08478039

CC Patent No. 5681732

CC GENERAL INFORMATION

CC APPLICANT: Newman, Roland A.

CC APPLICANT: Hanna, Nabil

CC APPLICANT: Paab, Ronald W.

CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy

CC NUMBER OF SEQUENCES: 114

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

CC STREET: 699 Prince St.

CC CITY: Alexandria

CC STATE: VA

CC COUNTRY: USA

CC ZIP: 22313-1404

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent in Release #1.0, Version #1.30

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08478.039

CC FILING DATE: 07-JUN-1995

CC CLASSIFICATION: 435

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/379,072

CC FILING DATE: 25-JAN-1995

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/912,292

CC FILING DATE: 10-JUL-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/856,281

CC FILING DATE: 23-MAR-1993

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/735,064

CC FILING DATE: 25-JUL-1991

CC ATTORNEY/AGENT INFORMATION:

QY 4 LLESGGLVLPKPSGLTSLCTVSGGSRSSHHWSVYRQPPGKGLWGEVFFSGSTIYNPS 63
Db 60 LRSRVMTSPDTKKNPFSVKITVTAADTAIYVCARETGTITETIS-NFFDIWGQGLT 118
QY 64 LNDRVMSVDKSDQVSLRSLSSVTAADTAIYVCARSPFMNQGPMMLDAFDIWGQGLT 123
Db 119 VSS 121
QY 124 VSS 126
RESULT 4
ID US-08-478-039-76 STANDARD: PRT: 125 AA.
XX XXXXXX
DT 01-JAN-1900
DE Sequence 76, Application US/08478039.
XX Sequence 76, Application US/08478039.
CC Patent No. 5681722
CC GENERAL INFORMATION:
CC APPLICANT: Newman, Roland A.
CC APPLICANT: Hanna, Nabil
CC APPLICANT: Paab, Ronald W
CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CC NUMBER OF SEQUENCES: 114
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
CC STREET: 699 Prince St.
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/478,039
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/379,072
CC FILING DATE: 25-JUL-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Teskin Esq., Robin L.
CC REGISTRATION NUMBER: 35,030
CC REFERENCE/DOCKET NUMBER: 012712-160
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-836-6620
CC TELEFAX: 703-836-2021
CC INFORMATION FOR SEQ ID NO. 76:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 125 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: not relevant
CC MOLECULE TYPE: peptide
CC ORIGINAL SOURCE:
CC ORGANISM: Monkey
CC POSITION IN GENOME:

CC CHROMOSOME/SEGMENT: VH4 clone 4-14
SQ SEQUENCE 125 AA: 13363 MW: 90929 CN:
Query Match 57.6%, Score 533, DB 7, Length 125;
Best Local Similarity 63.0%, Pred. No. 1, 29e-31;
Matches 80; Conservative 22; Mismatches 21; Indels 4; Gaps 4;
Db 1 QMOLOESGGLVLPKPSGLTSLCTCAVSGGSISSSYDWTWIRQPPGKGLWIAVSGNSGSAD 60
QY 1 EVOLLESGGLVLPKPSGLTSLCTVSGGSRSSHHWSVYRQPPGKGLWIGEVF-FSGSTI 59
Db 61 YNPGLNRTIISVDTSNNQPSLKMNTSVTAADTAIYVCARGDVT-S-GWYR-GYFDSWGG 117
QY 60 YNPGLNDRVMSVDKSDQVSLRSLSSVTAADTAIYVCARSPKMNQGRMLDAFDIWGOG 119
Db 118 CLVTSS 124
QY 120 TLVIVSS 126
RESULT 5
ID US-08-478-039-80 STANDARD: PRT: 121 AA.
XX XXXXXX
DT 01-JAN-1900
DE Sequence 80, Application US/08478039.
XX Sequence 80, Application US/08478039.
CC Patent No. 5681722
CC GENERAL INFORMATION:
CC APPLICANT: Newman, Roland A.
CC APPLICANT: Hanna, Nabil
CC APPLICANT: Paab, Ronald W
CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CC NUMBER OF SEQUENCES: 114
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
CC STREET: 699 Prince St.
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/478,039
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/379,072
CC FILING DATE: 25-JAN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/912,292
CC FILING DATE: 10-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/856,281
CC FILING DATE: 23-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/735,064
CC FILING DATE: 25-JUL-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Teskin Esq., Robin L.
CC REGISTRATION NUMBER: 35,030
CC REFERENCE/DOCKET NUMBER: 012712-160
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-836-6620
CC TELEFAX: 703-836-2021
CC INFORMATION FOR SEQ ID NO: 80:
CC POSITION IN GENOME:

US-08-844-215-6.rai

Thu Feb 26 07:06:11 1998

CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: not relevant
 CC TOPOLOGY: not relevant
 CC MOLECULE TYPE: peptide
 CC ORIGINAL SOURCE:
 CC ORGANISM: Monkey
 CC POSITION IN GENOME:
 CC CHROMOSOME/SEGMENT: VH4 anti-CD4 CHIM
 CC SEQUENCE 121 AA; 13232 MW; 88649 CN;
 SQ
 Query Match 56.2%; Score 520; DB 7; Length 121;
 Best Local Similarity 63.0%; Pred. No. 1.25e-30;
 Matches 80; Conservative 19; Mismatches 21; Indels 7; Gaps 5;
 Db 1 QVQLQAGPGLVPSQTLTLTCSVSGSGISGDIYWFIRQPPGKGLWIGVYGGSGGTN 60
 QY 1 EVQLLESGPGLVPSQTLTLTCTVSGSGISIRSSHWWSVVRQPPGKGLWIGVFFSGS-TI 59
 Db 61 YNPSSLNRRVSIISDTSKNLFSLKRSVTAAATVAVYCASNLKYLH-WL-L-Y--WGQG 114
 QY 60 YNPSSLNRRVSIISDTSKNLFSLKRSVTAAATVAVYCASNLKYLH-WL-L-Y--WGQG 119
 Db 115 VLTVSS 121
 QY 120 TLVIVSS 126
 RESULT 6
 ID US-08-478-039-108 STANDARD; PRT; 139 AA.
 XX
 AC xxxxxx
 XX 01-JAN-1900
 DT Sequence 108, Application US/08478039.
 DE
 XX Sequence 108, Application US/08478039
 CC Patent No. 5681722
 CC GENERAL INFORMATION:
 CC APPLICANT: Newman, Roland A.
 CC APPLICANT: Hanna, Nabil
 CC APPLICANT: Raab, Ronald W.
 CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
 CC NUMBER OF SEQUENCES: 114
 CC CORRESPONDENCE ADDRESSES:
 CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 CC STREET: 699 Prince St.
 CC CITY: Alexandria
 CC STATE: VA
 CC COUNTRY: USA
 CC ZIP: 22313-1404
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/478,039
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/379,072
 CC FILING DATE: 25-JAN-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/912,292
 CC FILING DATE: 10-JUL-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/856,281
 CC FILING DATE: 23-MAR-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/735,064

CC FILING DATE: 25-JUL-1991
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Teskin Esq., Robin L.
 CC REGISTRATION NUMBER: 35,030
 CC REFERENCE/DOCKET NUMBER: 012712-160
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 703-836-6620
 CC TELEFAX: 703-836-2021
 CC INFORMATION FOR SEQ ID NO: 108:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 139 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 139 AA; 15445 MW; 115855 CN;
 SQ
 Query Match 55.0%; Score 509; DB 7; Length 139;
 Best Local Similarity 61.9%; Pred. No. 8.66e-30;
 Matches 78; Conservative 20; Mismatches 21; Indels 7; Gaps 5;
 Db 20 QVQLQAGPGLVPSQTLTLTCSVSGSGISGDIYWFIRQPPGKGLWIGVYGGSGGTN 79
 QY 1 EVQLLESGPGLVPSQTLTLTCTVSGSGISIRSSHWWSVVRQPPGKGLWIGVFFSGS-TI 59
 Db 80 YNPSSLNRRVSIISDTSKNLFSLKRSVTAAATVAVYCASNLKYLH-WL-L-Y--WGQG 133
 QY 60 YNPSSLNRRVSIISDTSKNLFSLKRSVTAAATVAVYCASNLKYLH-WL-L-Y--WGQG 119
 Db 134 VLTVSS 139
 QY 120 TLVIVSS 125
 RESULT 7
 ID US-08-275-053-13 STANDARD; PRT; 121 AA.
 XX
 AC xxxxxx
 XX 01-JAN-1900
 DT Sequence 13, Application US/08275053.
 DE
 XX Sequence 13, Application US/08275053
 CC Patent No. 5607847
 CC GENERAL INFORMATION:
 CC APPLICANT:
 CC TITLE OF INVENTION: Recombinant human anti-human immunodeficiency
 CC NUMBER OF SEQUENCES: 16
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/275,053
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/CB93/01798
 CC INFORMATION FOR SEQ ID NO: 13:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 121 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 121 AA; 13365 MW; 86912 CN;
 SQ
 Query Match 54.7%; Score 506; DB 7; Length 121;
 Best Local Similarity 65.4%; Pred. No. 1.47e-29;
 Matches 83; Conservative 12; Mismatches 25; Indels 7; Gaps 4;
 Db 1 QVQLQAGPGLVPSQTLTLTCTVSGSGISIRSSHWWSVVRQPPGKGLWIGVYGGSGGTN 60
 QY 1 EVQLLESGPGLVPSQTLTLTCTVSGSGISIRSSHWWSVVRQPPGKGLWIGVFFSGS-TI 59

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Db      61 YPSPIKSVTMLRPTSKNOFSLSFSVTAQDAVYYCAPR---NHG-IT-TSMFYWQOG 114
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QY      60 YPNSLDDFVYFVSKDQVLSFSVTAADIAVYYCAPSDTKNNCGKPMQLDADF1WQGS 119
      1:1::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      115 SLVTYSS 121
      :|||:||||
QY      120 TLIVYSS 126
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RESULT	8
ID	US-08-111-080-28
XX	STANDARD:
AC	PRT: 120 AA
XXXXXX	
XX	
DT	01-JAN-1900
DT	
DE	Sequence 28, Application 08/111080.
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XX	Sequence 28, Application 08/111080
CC	Patent No. 5558865
CC	GENERAL INFORMATION:
CC	APPLICANT: Ohno, Tsuneva
CC	TITLE OF INVENTION: HIV Immunotherapeutics
CC	NUMBER OF SEQUENCES: 34
CC	CORRESPONDENCE ADDRESS:
CC	ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC	ADDRESSEE: Borun
CC	STREET: 6300 Sears Tower, ??? & Wacker Drive
CC	CITY: Chicago
CC	STATE: Illinois
CC	COUNTRY: USA
CC	ZIP: 60606
CC	COMPUTER READABLE FORM:
CC	MEDIUM TYPE: Floppy disk
CC	COMPUTER: IBM PC compatible
CC	OPERATING SYSTEM: PC-DOS/MS-DOS
CC	SOFTWARE: PatentIn Release #1.0, Version #1.25
CC	CURRENT APPLICATION DATA:
CC	APPLICATION NUMBER: 08/111,080
CC	FILING DATE:
CC	CLASSIFICATION: 424
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 07,748,562
CC	FILING DATE: 22-AUG-1991
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: PCT/US92/07111
CC	FILING DATE: 24-AUG-1992
CC	PRIOR APPLICATION DATA:
CC	APPLICATION NUMBER: US 08/039,457
CC	FILING DATE: 22-APP-1993
CC	ATTORNEY/AGENT INFORMATION:
CC	NAME: Borun, Michael F.
CC	REGISTRATION NUMBER: 25,447
CC	REFERENCE/DOCKET NUMBER: 31629
CC	TELECOMMUNICATION INFORMATION:
CC	TELEPHONE: (312) 474-6300
CC	TELEFAX: (312) 474-0448
CC	TELEX: 25-3856
CC	INFORMATION FOR SEQ ID NO: 28:
CC	SEQUENCE CHARACTERISTICS:
CC	LENGTH: 120 amino acids
CC	TYPE: amino acid
CC	TOPOLOGY: linear
CC	MOLECULE TYPE: protein
SQ	SEQUENCE 120 AA; 13278 MW; 84976 CN;

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QY      1 EVOLLESEPGVLKRSGLTSLICTVSGSSSTSSHW-WSWVRQPPKGLNIGVEFFSGSTLI 59
Db      61 YSPSIKSPVIMLPETSKNQFSLKSLSVIAATAVTYTCARE----NHG-TI-ISMIDWGGG 114
QY      60 YNPSLNIPVFEVSVKSKQVQVSLSLSVIAADTAVTYTCAPSPFKWNQGFMMLEADPIWGGG 119
Db      115 SLTVTS 120
QY      120 TLIVTS 125
PFSULT      9
ID      PCT-US93-07967-28      STANDARD;      PRT: 120 AA.
XX
XX      xxxxxx
DT      01-JAN-1900
XX
DE      Sequence 28, Application PC/TUS9307967.
XX
CC      Sequence 28, Application PC/TUS9307967
CC      GENERAL INFORMATION.
CC      APPLICANT: Ohno, Tsuneya
CC      TITLE OF INVENTION: HIV Immunotherapeutics
CC      NUMBER OF SEQUENCES: 34
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC      ADDRESSEE: Borun
CC      STREET: 6100 Sears Tower, 333 S Wacker Drive
CC      CITY: Chicago
CC      STATE: Illinois
CC      COUNTRY: USA
CC      ZIP: 60606
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: Floppy disk
CC      COMPUTER: IBM PC compatible
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: Patent In Release #1 0, Version #1.25
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US93/07967
CC      FILING DATE:
CC      CLASSIFICATION:
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: PCT/US92/07111
CC      FILING DATE: 24-AUG-1992
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/039,457
CC      FILING DATE: 22-APR-1993
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: Borun, Michael F.
CC      REGISTRATION NUMBER: 25,447
CC      REFERENCE/DOCKET NUMBER: 31629
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (312) 474-6300
CC      TELEFAX: (312) 474-0448
CC      TELEX: 25-3856
CC      INFORMATION FOR SEQ ID NO: 28:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 120 amino acids
CC      TYPE: amino acid
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 120 AA: 13378 MW: 94976 CN:

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Query Match          54.3%      Score 502; DB 6; Length 120;
Best Local Similarity 65.1%;    Pred. No. 2,96-29;
Matches             89; Conservative 12; Mismatches 35; Indels 7; Gaps 4;
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Matches	82	Conservative	12	W.matches	25	Indels	7	Gaps	8
Db	1	QVQLAESGPGLVRSQGLTSLTCTVSGFSTSSYCWHWVQPPGGLGIEWIGRICYEGSID	50						
QY	1	EVQLLESGPGLVKPSGTLTSLTCTVSGSGTSSPSHW-MSWVQPPGGLGIEWIGEVFVSSTI	59						
Db	61	YSPSTKSWIWLRIQTSKNOFSRLTSSVTAADIAVYVCARE----NHG-TT-TSMDYWGOG	114						

US-08-844-215-6.ra1

Thu Feb 26 07:06:11 1998

QY 60 YNPSLNDRVMSVDKSDQVSLRUSSVTAADTAVYYCARSPIKMNQGRMMLDAFDIWDGQ 119

Db 115 SLVTVS 120

QY 120 TLIVTS 125

RESULT 10
ID US-08-211-980-28 STANDARD: PRT: 120 AA.

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AC xxxxxx

XX 01-JAN-1900

DE Sequence 28, Application US/08211980.

XX Sequence 28, Application US/08211980.

CC Patent No 566556q

CC GENERAL INFORMATION:

CC APPLICANT: Ohno, Tsuneya

CC TITLE OF INVENTION: HIV Immunotherapeutics

CC NUMBER OF SEQUENCES: 38

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &

CC ADDRESSEE: Borun

CC STREET: 6300 Sears Tower, 233 S. Wacker Drive

CC CITY: Chicago

CC STATE: Illinois

CC COUNTRY: USA

CC ZIP: 60606

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: US/08/211,980

CC FILING DATE:

CC CLASSIFICATION: 424

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US92/07111

CC FILING DATE: 24-AUG-1992

CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 08/039,457

CC FILING DATE: 22-APR-1993

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Borun, Michael F.

CC REGISTRATION NUMBER: 25,447

CC REFERENCE/DOCKET NUMBER: 31629

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (312) 474-6300

CC TELEFAX: (312) 474-0448

CC INFORMATION FOR SEQ ID NO: 28:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 120 amino acids

CC TYPE: amino acid

CC TOPOLOGY: linear

CC MOLECULE TYPE: protein

CC SEQUENCE 120 AA; 13278 MW; 84976 CN;

Query Match 54.3%; Score 502; DB 7; Length 120;
Best Local Similarity 65.1%; Pred. No. 2.96e-29;
Matches 82; Conservative 12; Mismatches 25; Indels 7; Gaps 4;

Db 1 QVQLQESGPGLVKPSQTLSTCTVCSFSTSSSYCHWVRQPPGKCLEWIGRICEGSD 60

QY 1 EVQLLESGPGLVKPSGTLSLTCTVCSGSRSHW-WSWVRQPPGKLEWIGVFSGSTI 59

Db 61 YSPSIKSVTLMRLDTSKNQPSLTSVTAADTAVYYCARE---NHG-TT-TSMYDYGQ 114

QY 60 YNPSLNDRVMSVDKSDQVSLRUSSVTAADTAVYYCARSPIKMNQGRMMLDAFDIWDGQ 119

Db 115 SLVTVS 120

QY 120 TLIVTS 125

RESULT 11
ID PCT-US93-10555-16 STANDARD: PRT: 119 AA.

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AC xxxxxx

XX 01-JAN-1900

DE Sequence 16, Application PC/TUS9310555.

XX Sequence 16, Application PC/TUS9310555.

CC GENERAL INFORMATION:

CC APPLICANT: SILVERMAN, GREGG J.

CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF

CC TITLE OF INVENTION: VARIABLE REGION GENF FAMILY WESTRICTED ANTIBODIES

CC THROUGH

CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG

ATES

CC TITLE OF INVENTION: THEREOF

CC NUMBER OF SEQUENCES: 51

CC CORRESPONDENCE ADDRESS:

CC ADDRESSEE: Spensley Horn Jubas & Lubitz

CC STREET: 1880 Century Park East - Suite 500

CC CITY: Los Angeles

CC STATE: California

CC COUNTRY: USA

CC ZIP: 90067

CC COMPUTER READABLE FORM:

CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible

CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent In Release #1.0, Version #1.25

CC CURRENT APPLICATION DATA:

CC APPLICATION NUMBER: PCT/US93/10555

CC FILING DATE: 29-OCT-1993

CC CLASSIFICATION:

CC ATTORNEY/AGENT INFORMATION:

CC NAME: Howells, Stacy L.

CC REGISTRATION NUMBER: 34,842

CC REFERENCE/DOCKET NUMBER: FD-2630

CC TELECOMMUNICATION INFORMATION:

CC TELEPHONE: (619) 455-5100

CC TELEFAX: (619) 455-5110

CC INFORMATION FOR SEQ ID NO: 16:

CC SEQUENCE CHARACTERISTICS:

CC LENGTH: 119 amino acids

CC TYPE: amino acid

CC STRANDEDNESS: single

CC TOPOLOGY: linear

CC MOLECULE TYPE: peptide

CC IMMEDIATE SOURCE:

CC CLONE: LES

CC NAME/KEY: Peptide

CC LOCATION: 1..119

CC SEQUENCE 119 AA; 13135 MW; 76375 CN;

Query Match 54.1%; Score 500; DB 11; Length 119;
Best Local Similarity 62.5%; Pred No 4.20e-29;
Matches 75; Conservative 16; Mismatches 27; Indels 2; Gaps 2;

Db 1 QVQLQSGAGLLKFSSETLSLTCAYVGGPF-SGYVWSVYPPGKGPFWIRINISGHTTY 59

QY 1 EVQLLESGPGLVKP-SGLSLTCTVSGSIRSHW-SWVRQPPGKLEWIGVFSGSTIY 60

Db 60 NPSLTSRVMSLDTSKNQPSLTSVTAADTAVYYCARGPCEAVCTDAPCAVYCHWGQ 119

QY 61 NPSLNDRVMSVDKSDQVSLRUSSVTAADTAVYYCARSPIKMNQGRMMLDA-FDIWDGQ 119

RESULT 12 US-08-478-039-78 STANDARD: PFT: 124 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 78, Application US/08478039.
XX CC Sequence 78, Application US/08478039.
XX CC Patent No. 5681722
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Newman, Roland A.
XX CC APPLICANT: Hanna, Nabil
XX CC APPLICANT: Raab, Ronald W.
XX CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
XX CC NUMBER OF SEQUENCES: 114
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
XX CC STREET: 699 Prince St.
XX CC CITY: Alexandria
XX CC STATE: VA
XX CC COUNTRY: USA
XX CC ZIP: 22313-1404
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patent Release #1 0, Version #1 30
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/478.039
XX CC FILING DATE: 07-JUN-1995
XX CC CLASSIFICATION: 435
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/379,072
XX CC FILING DATE: 25-JAN-1995
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/912,292
XX CC FILING DATE: 10-JUL-1992
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/856,281
XX CC FILING DATE: 25-JUL-1991
XX CC NAME: Teskin Esq., Robin L.
XX CC REGISTRATION NUMBER: 35,030
XX CC REFERENCE/DOCKET NUMBER: 012712-160
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: 703-836-6620
XX CC TELEFAX: 703-836-2021
XX CC INFORMATION FOR SEQ ID NO: 78:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 124 amino acids
XX CC TYPE: amino acid
XX CC STRANDEDNESS: not relevant
XX CC TOPOLOGY: not relevant
XX CC MOLECULE TYPE: peptide
XX CC ORGANISM: Monkey
XX CC POSITION IN GENOME:
XX CC CHROMOSOME/SEGMENT: VH4 clone 4-16
XX CC SEQUENCE 124 AA: 13147 MW; 95091 CN;
Query Match 51.7%; Score 478; DB 7; Length 124;
Best Local Similarity 62.5%; Pred. No. 1.98e-27;
Matches 80; Conservative 14; Mismatches 27; Indels 7; Gaps 4;
Db 1 QVHLESGPGLVKPSTLSTLCVTSVSSGSISSGYYWGWIPQPGKGLWIGVFGSSGSI 60
1 EVOLLESGPGLVKPSTLSTLCVTSVSSGSISSGYYWGWIPQPGKGLWIGVFGSSGSI 58
61 SLNPSLKSRVTLSDVTSGNKFSLKSSVTAADTAATVFCAPF---LYSSSPY--TDFWGO 115
59 IYNPSLNCVFNVSVKDKVSLSSVTAADTAATVFCAPSPITKMGQGMMLTAEDINGO 118
116 GVRVTVSS 123
119 GTLVIVSS 126
RESULT 13
ID US-08-478-039-77 STANDARD: PFT: 119 AA.
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE Sequence 77, Application US/08478039.
XX CC Sequence 77, Application US/08478039
XX CC Patent No. 5681722
XX CC GENERAL INFORMATION:
XX CC APPLICANT: Newman, Roland A.
XX CC APPLICANT: Hanna, Nabil
XX CC APPLICANT: Raab, Ronald W.
XX CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
XX CC NUMBER OF SEQUENCES: 114
XX CC CORRESPONDENCE ADDRESS:
XX CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
XX CC STREET: 699 Prince St.
XX CC CITY: Alexandria
XX CC STATE: VA
XX CC COUNTRY: USA
XX CC ZIP: 22313-1404
XX CC COMPUTER READABLE FORM:
XX CC MEDIUM TYPE: Floppy disk
XX CC COMPUTER: IBM PC compatible
XX CC OPERATING SYSTEM: PC-DOS/MS-DOS
XX CC SOFTWARE: Patent Release #1 0, Version #1 30
XX CC CURRENT APPLICATION DATA:
XX CC APPLICATION NUMBER: US/08/478.039
XX CC FILING DATE: 07-JUN-1995
XX CC CLASSIFICATION: 435
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 08/379,072
XX CC FILING DATE: 25-JAN-1995
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/912,292
XX CC FILING DATE: 10-JUL-1992
XX CC PRIOR APPLICATION DATA:
XX CC APPLICATION NUMBER: US 07/856,281
XX CC FILING DATE: 25-JUL-1991
XX CC NAME: Teskin Esq., Robin L.
XX CC REGISTRATION NUMBER: 35,030
XX CC REFERENCE/DOCKET NUMBER: 012712-160
XX CC TELECOMMUNICATION INFORMATION:
XX CC TELEPHONE: 703-836-6620
XX CC TELEFAX: 703-836-2021
XX CC INFORMATION FOR SEQ ID NO: 77:
XX CC SEQUENCE CHARACTERISTICS:
XX CC LENGTH: 119 amino acids
XX CC TYPE: amino acid
XX CC STRANDEDNESS: not relevant
XX CC TOPOLOGY: not relevant
XX CC MOLECULE TYPE: peptide
XX CC ORIGINAL SOURCE:
XX CC ORGANISM: Monkey
XX CC POSITION IN GENOME:
XX CC CHROMOSOME/SEGMENT: VH4 clone 4-16
XX CC SEQUENCE 124 AA: 13147 MW; 95091 CN;

CC CHROMOSOME/SEGMENT: VH4 clone 4-14
SQ SEQUENCE 119 AA; 12636 MW; 81453 CN;

Query Match 51.1%; Score 473; DB 7; Length 119;
Best Local Similarity 68.7%; Pred. No. 4,75e-27;
Matches Conservative 11; Mismatches 19; Indels 1; Gaps 1;

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Yy 1 EVQLLESGPLVKPSGTLSLTCIVSGSISRSHWSVRQPFGKLEWIGEIVFSGSTIY 60

Dd 1 LNLCUKSRVTLSADTSKNQFSKLSSVTAADTAVYYCAR 99
| : | : | | | | | | : | : | | | | | | | | | |
Dd 1 NPSLNDRVFNSVDKSKDVSLRSLSSVTAADTAVYYCAR 98
Yy 1 -NPSLNDRVFNSVDKSKDVSLRSLSSVTAADTAVYYCAR 98

RESULT 14 STANDARD: PRT: 134 AA.

ID US-08-468-671-6
XX xxxxxx
AC
XX
DT 01-JAN-1900
XX Sequence 6, Application US/08468671.
DE Sequence 6, Application US/08468671.
XX Sequence 6, Application US/08468671
CC Patent No. 5648077
CC GENERAL INFORMATION:
CC APPLICANT: Ostberg, Lars G.
CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN
CC TITLE OF INVENTION: ANTIHOBIES SPECIFIC FOR HEPATITIS B SURFACE ANTIGEN

EN NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08468,671
CC FILING DATE: 06-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/259,372
CC FILING DATE: 14-JUN-1994
CC APPLICATION NUMBER: US 07/871,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/676,036
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/538,796
CC FILING DATE: 15-JUN-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/192,754
CC FILING DATE: 11-MAY-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/925,196
CC FILING DATE: 31-OCT-1986
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/904,517
CC FILING DATE: 05-SEP-1986
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William W.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-50-7

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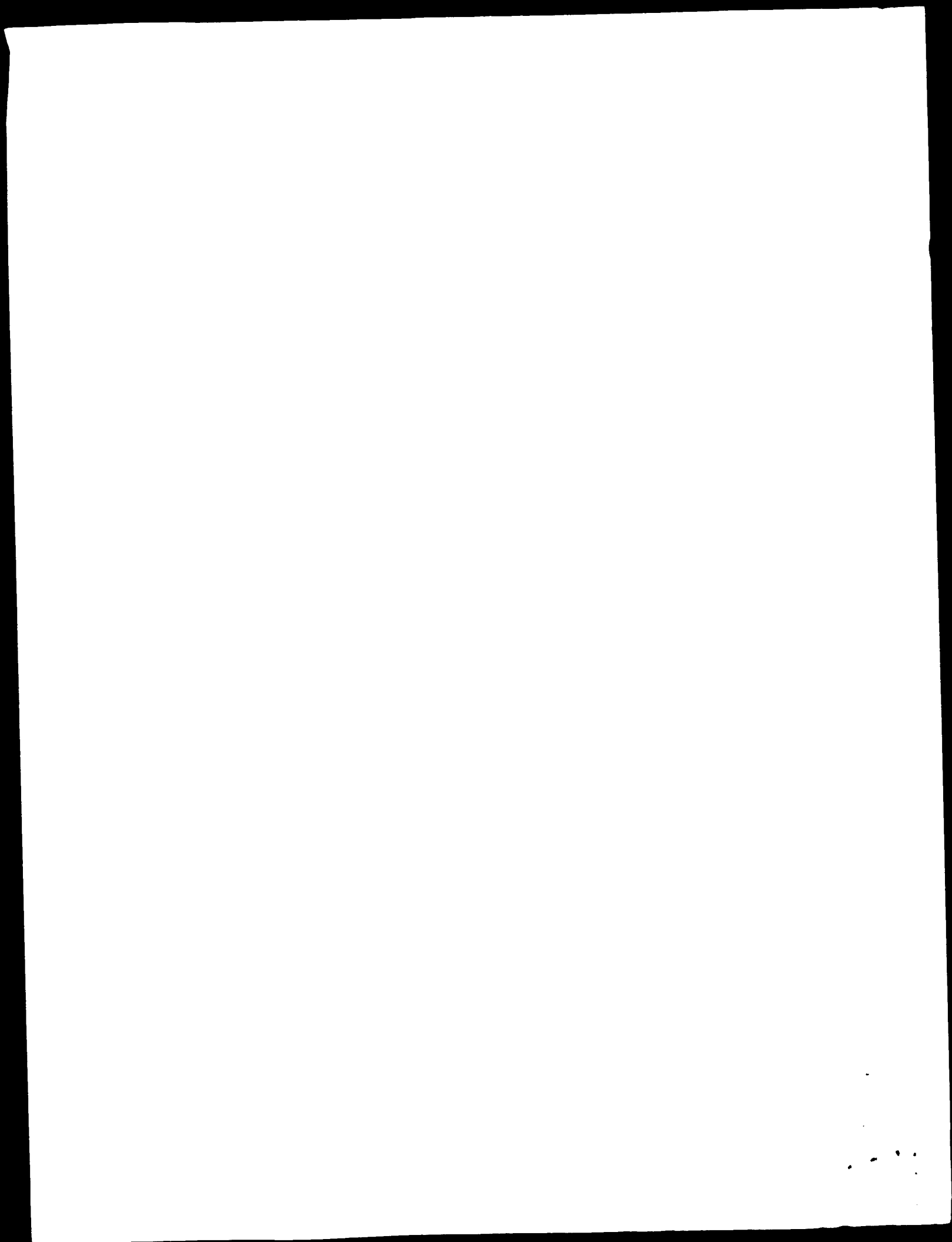
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 134 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 134 AA: 14995 MW: 109187 CN:

Query Match 50.9%; Score 471; DB 7; Length 134;
Best Local Similarity 69.7%; Pred. NO. 6.74e-27; Gaps 1;
Matches 69; Conservative 11; Mismatches 18; Indels 1;

20 QVQLSESGPLGVKAAETLSLCTVSRGSF-SDYFNNWFQPGAKREMLGRVYTSQSVDY 78
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1 EYQLSESGPLGVKPSGTLSTLCTVSGGSIKSHHMSWVRPPGKGLEWIGEVFTSGSTIY 60
: ||| ||| ||||| ||||| ||||| ||| : ||| ||||| ||||| ||| : ||| |
79 NPSLKSRTVTSYDTSKKQFSKLSSTVTDVADTAVYYCARG 117
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 NPSLNDRVPMFVDKSKDQVSLRSLSSVTADTAVYYCARS 99
||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15 STANDARD: PRT: 134 AA.
ID US-08-259-372A-6
XX xxxxxx
AC
XX
DT 01-JAN-1900
XX
DE Sequence 6, Application US/08259372A.
XX
Sequence 6, Application US/08259372A
CC Patent No. 5585354
CC GENERAL INFORMATION:
CC APPLICANT: Ostberg, Lars G.
CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
CC TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIG
CC EN
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/259,372A
CC FILING DATE: 14-JUN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/871,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/876,036
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/538,796
CC FILING DATE: 15-JUN-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/192,754
CC FILING DATE: 11-MAY-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/925,196
CC FILING DATE: 31-OCT-1986
CC PRIOR APPLICATION DATA:

```

WQESREH

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit,
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Mpsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:14:35 1998; MasPar time 6.79 Seconds
257.613 Million cell updates/sec

Tabular output not generated.
Title: >US-08-844-215-6
Description: (1-126) from US0844215 pep
Perfect Score: 925
Sequence: 1 EVOLLESGPGLVWPSTLSL ... PMMLDAFDWGGTILVSS 126

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq30
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
14:part14 15:part15 16:part16 17:part17 18:part18
19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 30.712; Variance 168.307; scale 0.182
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match Length	ID	Description
1	618	66.8	124 20	W06474 Human lung cancer spe
2	583	63.0	142 7	R41285 F105 rearranged varia
3	567	61.3	117 12	R66320 Human immunoglobulin
4	567	61.3	117 8	R40953 Human germ-line gene
5	559	60.4	124 2	R13266 Anti-human gHb F4C-1
6	558	60.3	127 2	P13265 Anti-human gHb F4C-R
7	558	60.3	475 16	P93553 Monoclonal antibody D
8	556	60.1	128 2	F13263 Anti-human gHb F4C-1
9	553	59.8	126 10	P54270 Anti-HIV gp41 immunog
10	553	59.8	126 19	W01315 Vh of Fab DL 41 19,
11	550	59.5	116 7	R42689 Vh 71-4.
12	550	59.5	116 12	R66346 Human immunoglobulin
13	550	59.5	476 20	W01922 Primatised anti-human
14	549	59.4	118 12	R66348 Human immunoglobulin
15	548	59.3	136 22	W24536 Immunoglobulin rB6B7
16	547	59.1	118 12	R66329 Human immunoglobulin
17	547	59.1	122 6	P30145 Mab 1-3-1 variable re
18	545	58.9	116 12	R66398 Human immunoglobulin
19	538	58.2	138 5	R29014 F4C-RVh-PM1f-4
20	539	58.2	138 5	R29017 F4C-RVh-PM1f

21	527	58.1	118 12	P66322 Human immunoglobulin
22	536	57.9	123 18	W03757 Anti-rhesus D monoclo
23	536	57.9	472 18	P33156 Anti-rhesus D recombi
24	531	57.4	872 19	W04102 Antibody/beta glucuro
25	529	57.2	119 6	P30143 Mab CAH variable regi
26	526	56.9	120 12	P66343 Human immunoglobulin
27	526	56.9	499 9	P50092 Humanised anti-CEA SF
28	525	56.8	117 7	P38660 Ab26
29	524	56.6	118 5	P29791 431/26 Vh hum
30	517	55.9	125 1	P81259 Variable region of hu
31	516	55.8	124 2	P12368 Anti-human gHb F4C-1
32	515	55.7	467 23	W14927 Human gamma-4E heavy
33	515	55.7	467 23	W14926 Human gamma-4E heavy
34	515	55.7	467 23	W14925 Human gamma-4E heavy
35	513	55.5	141 6	P31548 Anti-CD4 Vh peptide
36	509	55.0	119 23	W14772 Monkey anti-CD4 heavy
37	506	54.7	121 12	P65173 Region for producing
38	504	54.5	111 2	P12370 Anti-human gHb F4C-A
39	500	54.1	119 9	R54799 SPA-reactive IGM heav
40	499	53.9	116 12	P65124 Human immunoglobulin
41	495	53.5	119 23	W19876 CEA-specific antibody
42	492	53.2	114 12	R62319 Human cytomegalovirus
43	492	53.2	120 9	P48621 Sequence of the human
44	482	52.1	120 2	P11986 Human anti-placental
45	480	51.9	124 2	P70990 Sequence encoded by t

ALIGNMENTS

RESULT 1
ID W06474 standard: Protein: 124 AA.
AC W06474:
DT 23-MAY-1997 (first entry)
DE Human lung cancer specific antibody heavy chain variable region
KW Heavy chain; light chain; variable region; human; monoclonal antibody;
KW lung cancer tissue; diagnosis; purification; cancer-specific antigen; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..36
FT /label= CDR1
FT /note= "Fig 11, Claim 9"
FT Region 51..56
FT /label= CDR2
FT /note= "Fig 12, Claim 9"
FT Region 99..103
FT /label= CDR3
FT /note= "Fig 13, Claim 9"
PN J08280386-A.
PD 29-OCT-1996.
PF 14-APP-1995; 112671.
PF 14-APP-1995; JP-112671.
PA (MOMI) MORINAGA & CO LTD.
DR WPI: 97-014849/02.
DR N-PSDB: T45035.
FT Antibody specifically reactive to human lung cancer cells - also
FT corresponding DNA, used to diagnose cancer, or for purification of
FT cancer-specific antigen
PS Claim 3; Fig 3; 9pp; Japanese.
CC The sequences given in W06474-75 represents the heavy chain and light
CC chain variable regions from a human monoclonal antibody which is
CC specific for human lung cancer tissue. The monoclonal antibody may
CC be used for clinical diagnosis of cancer, for immunological therapy
CC or for purification of a cancer-specific antigen.
SQ Sequence 124 AA:

Query Match 66.8%; Score 618; DB 20; Length 124;
Best Local Similarity 71.4%; Pred. No. 5.59e-31;
Matches 90; Conservative 13; Mismatches 21; Indels 2; Gaps 1;
DB 1 EVOLLESGPGLVWPSTLSLTCIVS95SPSSHHNSWV4PPEKGLGLEISVFFSSTII 50
QY 1 EVOLLESGPGLVWPSTLSLTCIVS95SPSSHHNSWV4PPEKGLGLEISVFFSSTII 50

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PD 24-NOV-1994.
PF 10-MAY-1993; J06603.
PP 10-MAY-1993; W07080A3.
PA (NIBS ) JAPAN TOBACCO INC.
PB Honjo T., Matsuda F.
PC WPI: 95-006791/01.
PD N-PSDR: Q78966.
PE DNA fragment comprising human immunoglobulin Vh genes - for the
PF production of human immunoglobulin in mammalian hosts
PG Disclosure: Page 67-68; 130pp; Japanese.
PH Protein sequences (#66295-51) are novel human immunoglobulin heavy chain
PI sequences encoded by novel isolated genes. The genes (#78939-79002) Y21:
PJ isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;
PK Y6;Y24; 3-31; M8; M18 and M31. By PCR amplification using primers
PL Y6;Y24; 3-31; M8; M18 and M31. By PCR amplification using primers
PM Q78917-38. The genes are subdivided into 5 families of Vh genes. The
PN fragments cover a region of 800 kb. The cDNA fragments were isolated from
PO high molecular weight DNA from human placenta. The DNA was partially
PP digested with TaqI restriction enzyme. The fragments were separated by
PQ gel electrophoresis and 35-45 kb fractions were collected. The fragments
PR were ligated with ClaI-digested cosmid vector pJH81. The ligation
PS products were in vitro packed and infected into E.coli 490A. The
PT fragments were then subcloned by colony hybridisation. The Vh genes and
PU the DNA fragments encoding them are useful in producing human
PV immunoglobulin in mammalian hosts.
PW Sequence 117 AA:
PX
PY
PZ
QA Query Match 61 3%; Score 567; DR 12; Length 117;
QB Best Local Similarity 77.6%; Pred. No. 4,15e-33;
QC Matches 76; Conservative 11; Missmatch 11; Indels 0; Gaps 0;
QD
QE
QF
QG
QH
QI
QJ
QK
QL
QM
QN
QO
QP
QQ
QR
QS
QT
QU
QV
QW
QX
QY
QZ
RA RESULT
RB ID R40953 standard; protein; 117 AA.
RC AC R40953;
RD DT 25-FEB-1994 (first entry)
RE DE Human germ-line gene DP-68/JH6 antibody heavy chain.
RF KW humanised antibody; human germ-line; heavy chain; variable region;
RG framework region; reshaped antibody; CDR-grafted antibody;
RH complementarity determining region; immuno silent.
RI OS Homo sapiens.
RJ PH Key Location/Qualifiers
RK FT Region 1..26
RL FT /label= FR1
RM FT /note= "framework region"
RN FT Region 27..36
RO FT /label= CDR1
RP FT Region 37..50
RQ FT /label= FR2
RS FT /note= "framework region"
RT FT Region 51..66
RU FT /label= CDR2
RV FT Region 67 98
RW FT /label= FR3
RX FT /note= "framework region"
RY FT Region 69..106
RZ FT /label= CDR3
SA FT /label= FR4
SB FT /note= "framework region"
SC PN WC9317105-A.
SD PD 02-SEP-1993.
SE PF 19-FEB-1994; GU036d.
SF PR 19-FEB-1992; GB-003459.
SG PA (SCOT-) SCOTGEN LTD.
SH PI Carr FJ., Harris WJ. Winter GP;

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DR WPI: 93-288411/36.
PT New altered antibodies with reduced immune responses - have
PT germ-line aminoacid residues replacing somatically mutated
PT residues
PS Example 3; Fig 4a; 53pp; English.
CC A humanised antibody comprised CDRs originally from a mouse Mab
CC PSV19 specific for Respiratory Syncytial Virus transplanted onto
CC heavy and light chain V region domains derived from NEWM and REI
CC myeloma proteins, respectively. The framework regions of this
CC CDR-grafted antibody were converted to the germ-line equivalent
CC For conversion of the H-chain, the germ-line heavy chain DP68/JH6
CC (R40953) was used. Germ-line framework regions are those present in
CC immature B cells, i.e. prior to any somatic mutation which takes
CC place during maturation. Unlike mutations in the CDRs, any mutation
CC in framework regions does not affect affinity for an antigen and is
CC therefore essentially random. The mutation may, however, cause the
CC "self" antibody to be recognised as "foreign" and conversion to the
CC unmutated germ-line sequence renders the framework regions "immune
CC silent".
SQ Sequence 117 AA;

Query Match 61.3%; Score 567; DB 8; Length 117.
Best Local Similarity 77.6%; Pred. No. 4,15e-33;
Matches 76; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

Db 1 qvqlqesgpglvkpsdltscavsgysissnwwgwtgppdkglewgiyysgstyy 60
QY 1 EVQLLESGPGLVPSGTLSTLTCTVSGSGSPSSHHWWSWVPQPPKGLIEWIGVFSSGSIY 60

Db 61 npslndrvfmsvdkskdqvsulpslssvtaadtavvyycar 98
QY 61 NPSLNDRVFMSVDKSKDQVSLPSLSSVTAADTAVVYVCAP 99

RESULT 5
ID R12265 standard; Protein: 124 AA
AC R12265;
DE 15-AUG-1991 (first entry)
DE Anti-human RHD PAG-1 Mab (VH chain)
KW Monoclonal antibody; rhesus D; blood-typing; CDR;
KW haemolytic disease of the newborn; HDN.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50 65
FT /label= CDR2
FT Region 98 113
FT /label= CDR3
FT WO9107492-A.
PD 30-MAY-1991.
PF 13-NOV-1990; E01964.
PR 13-NOV-1989; GB-025590.
PA (BLOO-) CENT BLOOD LAB AUTH.
PI Hughes- Jones N;
PI WPI: 91-174104/24
PI N-PSDR: Q11948
PT DNA encoding complementary determining regions - of human
PT anti-rhesus D antibodies, useful in prodn. of monoclonal
PT antibodies and for passive immunisation
PS Disclosure: Fig 5, 32pp; English.
CC The DNA sequence of eleven monoclonal antibodies are
CC represented in Q119145-57. Synthetic genes, for both heavy and
CC light chains may be created by combining selected CDR 1, 2, and 3
CC regions, which may be selected from different antibody mols. having
CC varied binding specificity. The chimaeric anti-Rhd antibodies can be
CC used for diagnosis and therapy, and are capable of providing blood-
CC typing reagents of high specificity and reliability. They can also
CC be used in passive immunisation to prevent haemolytic disease of the
CC newborn.
SQ Sequence 124 AA;

Query Match 60.4%; Score 559; DB 2; Length 124;
Best Local Similarity 63.8%; Pred. No. 1.99e-32;
Matches 81; Conservative 18; Mismatches 27; Indels 1; Gaps 1;

Db 1 qlrlqesgpglvkpsdltscavsgysgsglykwgwwirppqkglewlgisfygssty 60
QY 1 EVQLLESGPGLVPSGTLSTLTCTVSGSGSISS-HHWWSWVPQPPKGLIEWIGVFSSGSIY 59

Db 61 npslndrvfmsvdkskdqvsulpslssvtaadtavvyycar 120
QY 60 YNPENLDRVFMVSKDKQVSLPSLSSVTAADTAVVYVCAPSIKMNQSPKMLDAFDIWSG 119

Db 121 tvtvss 127
QY 120 TLIVSS 126

RESULT 7
ID P0552 standard; Protein: 475 AA.

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Best Local Similarity 65.9%; Pred. No. 1.68e-32;
Matches 89; Conservative 15; Mismatches 26; Indels 2; Gaps 2;

Db 1 qvqlqesgpglvkpsdltscavsgysvssyw-swirgppdkgpegwigyysgstny 59
QY 1 EVQLLESGPGLVPSGTLSTLTCTVSGSGSISS-HHWWSWVPQPPKGLIEWIGVFSSGSIY 60

Db 60 npslndrvfmsvdkskdqvsulpslssvtaadtavvyycar 119
QY 61 NPSLNDRVFMSVDKSKDQVSLPSLSSVTAADTAVVYVCAPSIKMNQSPKMLDAFDIWSG 120

Db 119 tvtvss 124
QY 121 LVIVSS 126

RESULT 6
ID R12265 standard; Protein: 127 AA.
AC R12265;
DE 15-AUG-1991 (first entry)
DE Anti-human RHD R0G-B Mab (VH chain)
KW Monoclonal antibody; rhesus D; blood-typing; CDR;
KW haemolytic disease of the newborn; HDN.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..37
FT /label= CDR1
FT Region 52 67
FT /label= CDR2
FT Region 100..116
FT /label= CDR3
FT WO9107492-A.
PD 30-MAY-1991.
PF 13-NOV-1990; E01964.
PR 13-NOV-1989; GB-025590.
PA (BLOO-) CENT BLOOD LAB AUTH.
PI Hughes- Jones N;
PI WPI: 91-174104/24
PI N-PSDR: Q11947
PT DNA encoding complementary determining regions - of human
PT anti-rhesus D antibodies, useful in prodn. of monoclonal
PT antibodies and for passive immunisation
PS Disclosure: Fig 4; 32pp; English.
CC The DNA sequence of eleven monoclonal antibodies are
CC represented in Q119145-57. Synthetic genes, for both heavy and
CC light chains may be created by combining selected CDR 1, 2, and 3
CC regions, which may be selected from different antibody mols. having
CC varied binding specificity. The chimaeric anti-Rhd antibodies can be
CC used for diagnosis and therapy, and are capable of providing blood-
CC typing reagents of high specificity and reliability. They can also
CC be used in passive immunisation to prevent haemolytic disease of the
CC newborn.
SQ Sequence 127 AA;

Query Match 60.3%; Score 558; DB 2; Length 127;
Best Local Similarity 63.8%; Pred. No. 1.99e-32;
Matches 81; Conservative 18; Mismatches 27; Indels 1; Gaps 1;

Db 1 qlrlqesgpglvkpsdltscavsgysgsglykwgwwirppqkglewlgisfygssty 60
QY 1 EVQLLESGPGLVPSGTLSTLTCTVSGSGSISS-HHWWSWVPQPPKGLIEWIGVFSSGSIY 59

Db 61 npslndrvfmsvdkskdqvsulpslssvtaadtavvyycar 120
QY 60 YNPENLDRVFMVSKDKQVSLPSLSSVTAADTAVVYVCAPSIKMNQSPKMLDAFDIWSG 119

Db 121 tvtvss 127
QY 120 TLIVSS 126

RESULT 7
ID P0552 standard; Protein: 475 AA.

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R93553;
20-AUG-1996 (first entry)
DE Monoclonal antibody DNA heavy chain against 65 kD HCMV antigen.
KW Polymerase chain reaction; primer; amplification; PCR; light chain; MAB;
OS Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..19
FT /note= "Signal peptide"
FT Protein 20..475
FT /note= "Mature heavy chain"
PN J08038178-A.
PD 13-FEB-1996.
PF 20-FEB-1995; 030742.
PR 18-FEB-1994; JP-021628.
PA (NISHI) NISSHINBO IND INC.
PA (TANAKA) TANAKA H.
DR WPI: 96-154852/16.
DR N-PSDB; T18059.
PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
PT produced by primer amplification, used in the diagnosis of HCMV
PT infection.
PS Claim 4; Page 16-18; 22pp; Japanese.
CC The sequences given in R93553-54 represent the heavy and light chains
CC respectively of a monoclonal antibody against a 65 kD antigen of human
CC cytomegalovirus (HCMV). The DNA's encoding these sequences were
CC amplified using the sequences given in T18040-58. The monoclonal
CC antibody may be used in the diagnosis of HCMV.
SQ Sequence 475 AA;
Query Match 60.3%; Score 558; DB 16; Length 475;
Best Local Similarity 66.4%; Pred. No. 1.99e-32;
Matches 85; Conservative 18; Mismatches 21; Indels 4; Gaps 3;
Db 20 qlqlqsgqglvkpsetlsitctvsgdsisrsgysgcirppqgkglewigtivysgsty 79
QY 1 EVOLLESGPGLVKPSTLSITCTVSGSIS-RSSHMSWVRQPPGKGLEWIGVFSGSTI 59
Db 80 ynpslksrvtisvdaannqfslklssvtadtaavyycartspqyyd--lltgsfpywqq 137
QY 60 YNPSLNDRVFMSVDKSDQVSLSSVTAAATAVYYCARSPKMNQGRMM--LDAF-DIMG 118
Db 138 qltlvtvss 145
QY 119 GTLIVVSS 126
RESULT 8
ID R12269 standard; Protein: 128 AA.
AC R12269;
DE Anti-human RhD FOM-1 MAB (VH chain).
KW Monoclonal antibody; rhesus D; blood-typing; CDR;
KW haemolytic disease of the newborn; HDN.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50..65
FT /label= CDR2
FT Region 98..117
FT /label= CDR3
FN WO9107492-A.
PD 30-MAY-1991.
PF 13-NOV-1990; E01964.
PR 13-NOV-1989; GB-025590.
PA (BLOO) CENT BLOOD LAB AUTH.
PI Hughes-Jones N;
DR WPI: 91-178104/24.
DR N-PSDB; Q11951.
PT DNA encoding complementary determining regions of human
PT anti-rhesus D antibodies, useful in prodn. of monoclonal
PT antibodies and for passive immunisation

PS Disclosure; Fig 8; 32pp; English.
CC The DNA sequence of eleven monoclonal antibodies are
CC represented in Q119145-57. Synthetic genes, for both heavy and
CC light chains may be created by combining selected CDR 1, 2, and 3
CC regions, which may be selected from different antibody mols. having
CC varied binding specificity. The chimeric anti-RhD antibodies can be
CC used for diagnosis and therapy, and are capable of providing blood-
CC typing reagents of high specificity and reliability. They can also
CC be used in passive immunisation to prevent haemolytic disease of the
CC newborn.
SQ Sequence 128 AA;
Query Match 60.1%; Score 556; DB 2; Length 128;
Best Local Similarity 62.8%; Pred. No. 2.83e-32;
Matches 81; Conservative 22; Mismatches 22; Indels 4; Gaps 3;
Db 1 qvqlqgqgllkpksetlsitcavvggsf-sgyvwnwirppqkalewlgelhsqstny 59
QY 1 EVOLLESGPGLVKPSTLSITCTVSGSISPSHMSWVRQPPGKGLEWIGVFSGSTI 60
Db 60 npslksrvtmsvdtksnqfslklssvtadtaavyycartspqyyd--lltgsfpywqq 119
QY 61 NPSLNDRVFMSVDKSDQVSLSSVTAAATAVYYCARSPKMNQGRMM--LDAF-DIMG 117
Db 120 kattvtvss 128
QY 118 QGTLIVVSS 126
RESULT 9
ID R54270 standard; Protein: 126 AA.
AC R54270;
DE Anti-HIV gp41 immunoglobulin heavy chain V region clone pl. 41.19.
KW Human immunodeficiency virus; HIV1; glycoprotein gp41; epitope;
KW neutralisation; Monoclonal antibody; heavy chain; variable region;
KW framework region; complementarity determining region.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 1..27
FT /label= FR1
FT Region 28..32
FT /label= CDR1
FT Region 33..46
FT /label= FR2
FT Region 47..62
FT /label= CDR2
FT Region 63..94
FT /label= FR3
FT Region 95..110
FT /label= CDR3
FT Region 111..126
FN WO9407922-A.
PD 14-APR-1994.
PF 30-SEP-1993; U09328.
PR 30-SEP-1992; US-954148.
PA (SCRI) SCRIPPS RES INST.
PA Barbas CF, Burton DR, Lerner RA;
PI WPI: 94-135516/16.
DR New human monoclonal antibodies neutralising HIV - react with
DR gp120 or gp41 and nucleic acid encoding them, useful for in vivo
DR or in vitro diagnosis and for passive immunotherapy
PS Claim 9; Page 212; 248pp; English.
CC Lymphocyte mRNA was converted to cDNA and subjected to PCR
CC amplification using primers specific for heavy and light chain
CC variable regions. The amplification products were inserted into a
CC dicistronic vector to produce a library of fragments. E.coli XL1
CC Blue cells were transformed with the library. Filamentous phage were
CC produced which expressed the MAB regions on their surface. Panning
CC with gp120 and gp41 resulted in the recovery of immunoreactive
CC clones. The heavy chain VH region sequence R54270 neutralises HIV1
CC gp41.

SQ Sequence 126 AA:

Query Match 59.8%; Score 553; DB 10; Length 126;
 Best Local Similarity 56.7%; Pred. No. 4, 778-82;
 Matches 82; Conservative 14; Mismatches 25; Indels 2; Gaps 2;

Db 1 llesgplvlpsetlsictvsgsissfdw-nwirgpaqkalewigriypsgnthynps 59
 QY 4 LLESGPLVLPSETLSICTVSGSISRSHHWSWVQPPKGLEWIGEVFFSGSTIYNPS 63
 Db 60 lrsrvmtsdtsknqfsvkltsytaadtalyccarentgtrtleeig-nffdiwgqgtlvt 118
 QY 64 LNDRVFMSVDKSDQVSLRSSVTAADTAVVYCAPSPIKWNCGPMMLDAFDWQGTTLVI 123
 Db 119 vss 121
 QY 124 VSS 126

RESULT 10

ID W01315 standard; Protein: 126 AA

AC W01315; 1997 (first entry)

DE VH of Fab DL 41 19, binds to HIV gp41.

KW Heavy chain; light chain; variable region; VH; monoclonal antibody;

KW MAb; HIV; human immunodeficiency virus; glycoprotein; gp120; clone;

KW virus infectivity assay; precursor gp160; immunocompetence; human;

KW anti-HIV antibody; detection; HIV infection.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 1..27

FT /label= FR1

FT Region 28..32

FT /label= CDR1

FT Region 33..46

FT /label= FR2

FT Region 47..52

FT /label= CDR2

FT Region 63..94

FT /label= FR3

FT Region 95..110

FT /label= CDR3

FT Region 111..126

FT /label= FR4

PN W09602273-A1.

PD 01-FEB-1996

PF 11-JUL-1995; U08743.

PR 18-JUL-1994; US-276852.

PA (SCR1) SCRIPPS RES INST.

PI Barbas CF, Burton DR, Lerner RA;

DR WPI: 96-179601/18.

PT Monoclonal antibody binding to V1/V2 loop of HIV gp120 - used in

PT passive immunotherapy and detection of HIV infection.

PS Example 3; Fig 18; 366pp; English.

CC The sequences given in W01315-19 represent the heavy chain variable

CC regions (VH) of a series of antibody fragments (FAB's) which are

CC immunoreactive with HIV glycoprotein gp41. This sequence represents

CC the sequence of the clone, DL 41 19. These sequences represent heavy

CC chains which bind to the light chain clones given in W01320-24. A

CC monoclonal antibody containing one of these Fab sequences may have the

CC capacity to reduce HIV infectivity titre in an in vivo virus infectivity

CC assay by 50 % at a concentration of less than 700 ng of antibody/ml.

CC The MAb may be used for determining immunocompetence of a human anti-HIV

CC antibody and in the detection of HIV infection.

SQ Sequence 126 AA;

Query Match 59.8%; Score 553; DB 19; Length 126;

Best Local Similarity 56.7%; Pred. No. 4, 778-82;

Matches 82; Conservative 14; Mismatches 25; Indels 2; Gaps 2;

Db 1 llesgplvlpsetlsictvsgsissfdw-nwirgpaqkalewigriypsgnthynps 59
 QY 4 LLESGPLVLPSETLSICTVSGSISRSHHWSWVQPPKGLEWIGEVFFSGSTIYNPS 63

Db 60 lrsrvmtsdtsknqfsvkltsytaadtalyccarentgtrtleeig-nffdiwgqgtlvt 118
 QY 64 LNDRVFMSVDKSDQVSLRSSVTAADTAVVYCAPSPIKWNCGPMMLDAFDWQGTTLVI 123
 Db 119 vss 121
 QY 124 VSS 126

RESULT 11

ID R42689 standard; Protein: 116 AA

AC R42689;

DT 01-NOV-1993 (first entry)

DE Vh 71-4.

KW Monoclonal antibody, MAb; envelope, glycoprotein; gp120. HIV, AIDS;

KW CD4; receptor; hybridoma; polymerase chain reaction; PCR; heavy; light;

KW chain; epitope; immune deficiency.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..19

FT /label= sig_peptide

FT Protein 20..116

FT /label= mat_protein

FT Region 49..54

FT /label= CDR1

FT Region 69..84

FT /label= CDR2

PN W09312233-A.

PD 24-JUN-1993.

PF 10-DEC-1992; U10928.

PR 10-DEC-1991; US-804652.

PA (DAND) DANA FAPREP CANCER INST INC.

PA (NEWSE-) NEW ENGLAND DEACONNESS HOSPITAL CORP.

PI Haseltine WA, Marasco WA, Posner MP, Sodroski JG;

DR WPI: 93-214174/26.

DR N-FCDB: Q42697.

FT DNA segments encoding monoclonal antibody - which binds to gp120

FT and neutralises HIV, for treating AIDS, and for diagnosing and

FT monitoring HIV infection

PS Disclosure; Page 64; 109pp; English.

CC The nucleotide sequence of rearranged F105 Vh (Q42698) was compared

CC to two monoclonal antibodies (Ab26 - Q42702) and 288-D - Q42703).

CC which by nucleotide sequence analysis, appear to use a rearranged

CC Vh 71-4 gene (Q42697).

CC Ab26 (Q42702) was derived from CD5+ B cells of a healthy donor and

CC represents a naturally occurring polyclonal antibody which binds to

CC many antigens. Ab26 shares greatest sequence similarity with germline

CC Vh 71-4.

SQ Sequence 116 AA;

Query Match 59.5%; Score 550; DB 7; Length 116;

Best Local Similarity 78.6%; Pred. No. 8 04e-32;

Matches 77; Conservative 10; Mismatches 10; Indels 1; Gaps 1;

Db 20 qvqlgesgplvlpsetlsictvsgsissfdw-nwirgpaqkalewigriypsgntny 78
 QY 1 EVQLLESGPLVLPSETLSICTVSGSISRSHHWSWVQPPKGLEWIGEVFFSGSTIY 60

Db 79 npslksrvtlsvdtskqfalklssttaadtavvyar 116

QY 61 NPSLKSrvtlsvdtskqfalklssttaadtavvyar 98

RESULT 12

ID R66346 standard; Protein: 116 AA.

AC R66346;

DT 04-AUG-1995 (first entry)

DE Human immunoglobulin; variable heavy chain #52.

KW Primer; PCR; amplify; human; immunoglobulin; variable; heavy chain.

KW cosmid; placenta; vector; pDB81; E.Coli; mammalian.

OS Homo sapiens.

PN W09425895-A.

```

CC and graft-versus-host disease.
SQ Sequence 476 AA:

Query Match 59.5%; Score 550; DB 20; Length 476;
Best Local Similarity 52.5%; Pred. No. 8,046-32;
Matches 80; Conservative 19; Mismatches 26; Indels 3; Gaps 4;

Db 20 qvqlqespgplvkpsetlsitcavsgsgsgyqgwirqpakulewidsyfsassnt 79
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGPGLVSPGDTLTCTIVSGSIRSSHHWSWVROPFGKLEWICEVFFSGST 59
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 80 ynpkslqsvtistdsknqfsiklsmtaadtavyycvdrflfsvwg-myyvnnwfdwq 138
      |||||: :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 YNPSLNDRVFMVDKSKDQVSLRSLSVTAADTAVYYCARSPFKMNQGHMLDA-FDIW 118
      |||||: :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 139 qvltvss 146
      |||||: |||||
QY 119 GTLVIVSS 126
      |||||: |||||

RESULT 14
ID R66348 standard; Protein: 118 AA.
AC R66348;
DT 04-AUG-1995 (first entry)
DE Human immunoglobulin variable heavy chain #54.
KW primer; PCR; amplification; human; immunoglobulin; variable; heavy chain;
KW cosmid; placenta; vector; pJB81; E.coli; mammalian.
KW Homo sapiens.
PN W09426895-A
PD 24-NOV-1994.
PF 10-MAY-1993; J00603.
PP 10-MAY-1993; W0100603.
PR (N15) JAPAN TOBACCO INC.
PA Honjo T., Matsuda F.
PI WPI: 95-006791/01.
DR NP-SDB; Q78999.
DT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
PS disclosure; page 110-111; 130pp; Japanese.
CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
CC sequences encoded by novel isolated genes. The genes (Q78949-79002) were
CC isolated and cloned from a series of cosmid constructions. Y202; Y103; Y21;
CC Y6; Y24; 3-31; M8; M18 and M131, by PCR amplification using primers
CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
CC fragments cover a region of 800 kb. The DNA fragments were isolated from
CC high molecular weight DNA from human placenta. The DNA was partially
CC digested with TaqI restriction enzyme. The fragments were separated by
CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
CC were ligated with ClaI-digested cosmid vector pJB81. The ligation
CC products were in vitro packed and infected into E.coli 490A. The
CC fragments were then subcloned by colony hybridisation. The Vh genes and
CC immunoglobulin in mammalian hosts.
SQ Sequence 118 AA:

Query Match 59.4%; Score 549; DB 12; Length 118;
Best Local Similarity 77.8%; Pred. No. 9,576-12;
Matches 77; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

Db 20 qvqlqespgplvkpsetlsitcavsgsgsgyqgwirqpakulewidsyfsassnt 79
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGPGLVSPGDTLTCTIVSGSIRSSHHWSWVROPFGKLEWICEVFFSGST 59
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 80 ynpkslqsvtistdsknqfsiklsmtaadtavyyccar 118
      |||||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 YNPSLNDRVFMVDKSKDQVSLRSLSVTAADTAVYYCAR 98
      |||||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 15
ID W24536 standard; Protein: 136 AA.
AC W24536;
DT 09-OCT-1997 (first entry)
DE Immunoglobulin RB67 heavy chain variable region.
PF Honjo T., Matsuda F.
PI WPI: 95-006791/01.
DR NP-SDB; Q78999.
DT DNA fragment comprising human immunoglobulin Vh genes - for the
PT production of human immunoglobulin in mammalian hosts
PS disclosure; page 110-111; 130pp; Japanese.
CC Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
CC sequences encoded by novel isolated genes. The genes (Q78949-79002) were
CC isolated and cloned from a series of cosmid constructions. Y202; Y103; Y21;
CC Y6; Y24; 3-31; M8; M18 and M131, by PCR amplification using primers
CC Q78917-38. The genes are subdivided into 5 families of Vh genes. The
CC fragments cover a region of 800 kb. The DNA fragments were isolated from
CC high molecular weight DNA from human placenta. The DNA was partially
CC digested with TaqI restriction enzyme. The fragments were separated by
CC gel electrophoresis and 35-45 kb fractions were collected. The fragments
CC were ligated with ClaI-digested cosmid vector pJB81. The ligation
CC products were in vitro packed and infected into E.coli 490A. The
CC fragments were then subcloned by colony hybridisation. The Vh genes and
CC immunoglobulin in mammalian hosts.
SQ Sequence 118 AA:

Query Match 59.4%; Score 549; DB 12; Length 118;
Best Local Similarity 77.8%; Pred. No. 9,576-12;
Matches 77; Conservative 10; Mismatches 11; Indels 1; Gaps 1;

Db 20 qvqlqespgplvkpsetlsitcavsgsgsgyqgwirqpakulewidsyfsassnt 79
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGPGLVSPGDTLTCTIVSGSIRSSHHWSWVROPFGKLEWICEVFFSGST 59
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 80 ynpkslqsvtistdsknqfsiklsmtaadtavyyccar 118
      |||||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 YNPSLNDRVFMVDKSKDQVSLRSLSVTAADTAVYYCAR 98
      |||||: |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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24-NOV-1994.
10-MAY-1993; J00603.
10-MAY-1993; W0-J00603.
(NIBS) JAPAN TOBACCO INC.
Honjo T, Matsuda F;
WPI: 95-006791/01.
N-PSDB; T89997.
DNA fragment comprising human immunoglobulin Vh genes - for the
production of human immunoglobulin in mammalian hosts
Disclosure; Page 107-108; l3Opp; Japanese.
Protein sequences (R66295-51) are novel human immunoglobulin heavy chain
sequences encoded by novel isolated genes. The genes (G789q9-79002) were
isolated and cloned from a series of cosmid constructs: Y202; Y103; Y21;
Y6; Y24; 3-31; M84; M18 and M131, by PCR amplification using primers
G78917-38. The genes are subdivided into 5 families of Vh genes. The
fragments cover a region of 800 kb. The DNA fragments were isolated from
high molecular weight DNA from human placenta. The DNA was partially
digested with Taqi restriction enzyme. The fragments were separated by
gel electrophoresis and 35-45 kb fractions were collected. The fragments
were ligated with ClaI-digested cosmid vector pJB81. The ligation
products were in vitro packed and infected into E.coli 450A. The
fragments were then subcloned by colony hybridisation. The vH genes and
the DNA fragments encoding them are useful in producing human
immunoglobulin in mammalian hosts.

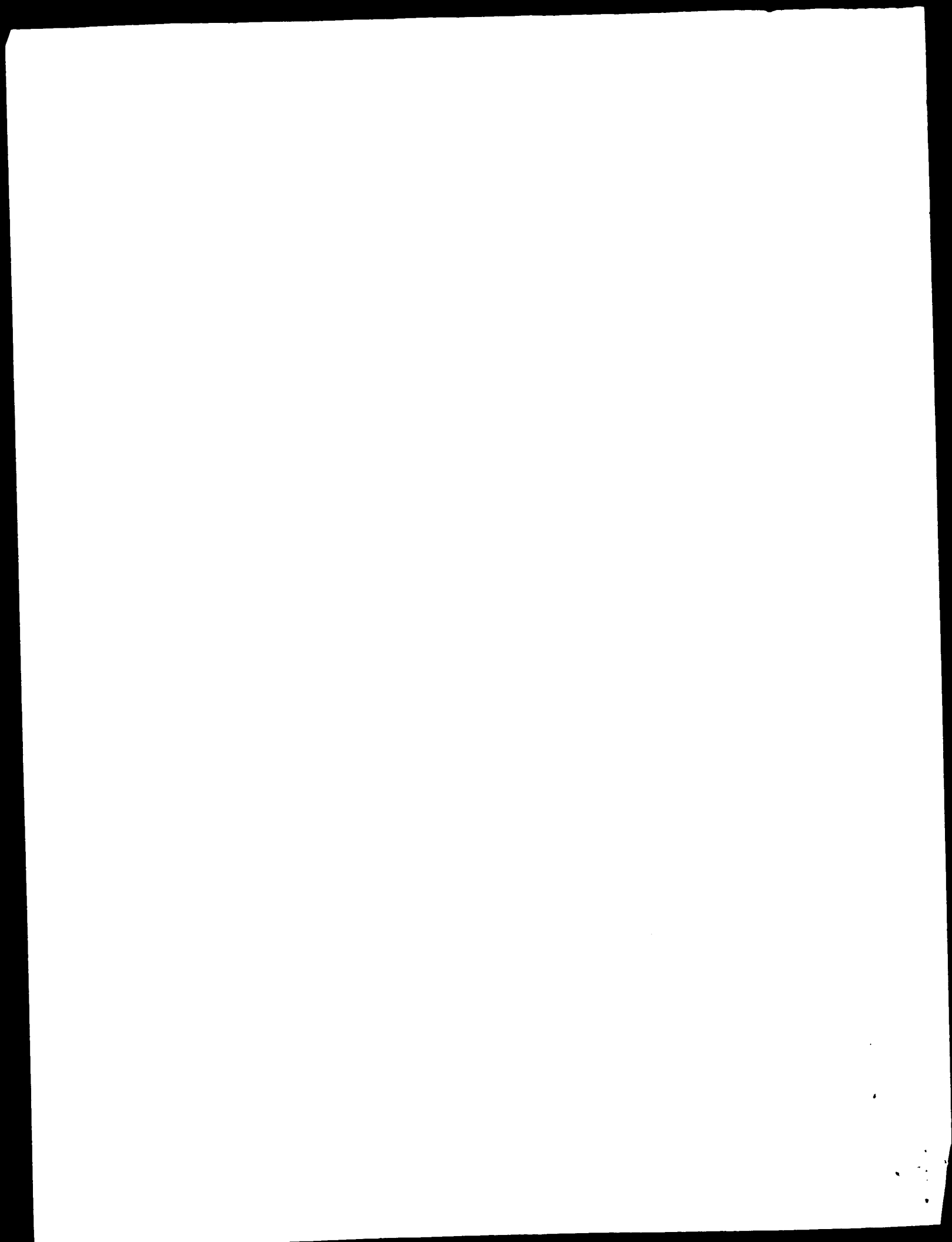
Query Match 59.5%; Score 550; DB 12; Length 116;
Best Local Similarity 78.8%; Pred No. 8, 04e-32;
Matches 77; Conservative 10; Mismatches 10; Indels 1; Gaps 1.

Db 20 qvqlqesgpglvkxpseltlctvtggav-syyyswlrpppkglewlglyygsstny 78
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1 EVQLLESGPGLVKPSGTLSLTCTVCGSRSSHMWSWRPPKGLEWIGVEFGSGTIY 60

Db 79 npsksrvtlsvdtsknqfslklssvytaadtavyycar 116
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61 NPSLNDVRFMVSVDKSKDQSVSLRSSVTADTAVYYCAR 98

RESULT 13
ID W01822 standard; Protein; 476 AA.
AC W01822;
DT 25-MAY-1997 (first entry)
DE Primatised anti-human B7.1 antigen antibody 16C10 heavy chain.
KW Monoclonal antibody; cynomolgus monkey; macaque; 16C10.
KW Primatised antibody; B7 antigen; CD28; immunosuppressive;
KW autoimmune disease; idiopathic thrombocytopaenia purpura;
KW systemic lupus erythematosus; rheumatoid arthritis; psoriasis;
KW type 1 diabetes mellitus; graft versus host disease;
KW hetero-hybridoma; transfectoma.
OS Chimeric Macaca cynomolgus;
OS Chimeric Homo sapiens.
PN W09640878-A1.
PD 19-DEC-1996.
PF 06-JUN-1986; U10053.
PR 07-JUN-1995; US-487550.
PA (IDEC-) IDEC PHARM CORP.
PI Anderson DR, Brams P, Hanna N, Shestowsky WS;
DR WPI: 97-108638/10.
DR N-PSDB; T62513.
PT Monkey monoclonal antibody binding human B7.1 or B7.2 antigen -
PT useful for treating autoimmune disease or graft-versus-host disease
PS Claim 14, Fig 10B; 81pp; English.
PS 2 polypeptides (W01821 and W01822) respectively comprise primatised
CC forms of the light and heavy chains of cynomolgus monkey anti-human
CC B7.1 antigen monoclonal antibody 16C10. Cloned 16C10 light and
CC heavy variable genes (see also T62512 and T62513) are inserted into
CC an expression vector (ref. NEOSPLA) which contains human light and
CC heavy chain constant region genes to allow prodn. of the primatised
CC antibody in e.g. CHO cells. Primatised 7C10 and 786 anti-B7.1
CC antibodies have also been produced (see also W01817-20). The
CC primatised antibodies inhibit the B7/CD28 pathway, making them
CC useful immunosuppressants for the treatment of autoimmune disorders

Search completed: Tue Feb 24 07:15:06 1998
Job time : 31 secs.



WQRELE (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on Tue Feb 24 07:11:04 1998; MasPar time 7.28 seconds
361 213 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-5
Description: (1-124) from US08844215.pep
Perfect Score: 926
Sequence: 1 EVOLLEGGGSGWQPGPSLPL IKRYYLENWGGTLVTYSS 124

Scoring table: PAM 150
Gap 11

Searched: 59021 seqs, 21210388 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2 part2 3 part3 4 part4 5 part5 6 part6 7 part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 42.049; Variance 78.185; scale 0.538

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	700	75.6	122	5	HV3G_HUMAN IG HEAVY CHAIN V-III	2.75e-124
2	679	73.3	121	5	HV3J_HUMAN IG HEAVY CHAIN V-III	1.15e-119
3	676	73.0	122	5	HV3H_HUMAN IG HEAVY CHAIN V-III	5.23e-119
4	669	72.2	126	5	HV3K_HUMAN IG HEAVY CHAIN V-III	1.80e-117
5	636	68.7	119	5	HV3L_HUMAN IG HEAVY CHAIN V-III	3.09e-110
6	610	65.9	119	5	HV3C_HUMAN IG HEAVY CHAIN V-III	1.49e-104
7	598	64.6	117	5	HV3E_HUMAN IG HEAVY CHAIN V-III	6.16e-102
8	593	63.5	120	5	HV3F_HUMAN IG HEAVY CHAIN V-III	7.57e-101
9	588	63.5	120	5	HV3D_HUMAN IG HEAVY CHAIN V-III	9.28e-100
10	584	63.1	122	5	HV3A_HUMAN IG HEAVY CHAIN V-III	6.80e-99
11	577	62.3	126	5	HV3G_MOUSE IG HEAVY CHAIN V-III	2.26e-97
12	575	62.1	119	5	HV3N_HUMAN IG HEAVY CHAIN V-III	6.23e-97
13	570	61.6	116	5	HV3T_HUMAN IG HEAVY CHAIN V-III	7.60e-96
14	563	60.8	114	5	HV3M_HUMAN IG HEAVY CHAIN V-III	2.51e-94
15	554	59.8	115	5	HV3P_HUMAN IG HEAVY CHAIN V-III	2.25e-92
16	553	59.7	115	5	HV3D_HUMAN IG HEAVY CHAIN V-III	3.70e-92
17	551	59.5	116	5	HV3S_HUMAN IG HEAVY CHAIN V-III	1.00e-91
18	546	59.0	119	5	HV3P_HUMAN IG HEAVY CHAIN V-III	1.21e-90
19	546	59.0	142	5	HV3I_HUMAN IG HEAVY CHAIN V-III	1.21e-90
20	543	58.6	114	5	HV3E_HUMAN IG HEAVY CHAIN V-III	5.41e-90
21	542	58.5	123	5	HV3S_MOUSE IG HEAVY CHAIN V-III	8.91e-90
22	542	58.5	123	5	HV3E_MOUSE IG HEAVY CHAIN V-III	8.91e-90

22	542	59.5	123	5	HV3S_MOUSE IG HEAVY CHAIN V-III	8.91e-90
24	539	59.2	123	5	HV3E_MOUSE IG HEAVY CHAIN V-III	3.97e-89
25	538	59.1	117	5	HV3Q_HUMAN IG HEAVY CHAIN V-III	6.53e-89
26	536	57.9	97	5	HV5G_MOUSE IG HEAVY CHAIN V-III	1.77e-88
27	536	57.9	122	5	HV2Q_MOUSE IG HEAVY CHAIN V-III	2.12e-87
28	531	57.3	117	5	HV3Q_HUMAN IG HEAVY CHAIN V-III	2.12e-87
29	531	57.3	123	5	HV3E_MOUSE IG HEAVY CHAIN V-III	3.12e-87
30	530	57.2	117	5	HV5S_MOUSE IG HEAVY CHAIN V-III	3.49e-87
31	530	57.2	123	5	HV2S_MOUSE IG HEAVY CHAIN V-III	3.49e-87
32	527	56.9	122	5	HV2I_MOUSE IG HEAVY CHAIN V-III	1.55e-86
33	526	56.8	117	5	HV54_MOUSE IG HEAVY CHAIN V-III	2.55e-86
34	526	56.8	144	5	HV26_MOUSE IG HEAVY CHAIN V-III	2.55e-86
35	525	56.7	98	5	HV57_MOUSE IG HEAVY CHAIN V-III	4.19e-86
36	520	56.2	117	5	HV3L_MOUSE IG HEAVY CHAIN V-III	5.02e-85
37	519	56.0	144	5	HV3I_MOUSE IG HEAVY CHAIN V-III	8.25e-85
38	516	55.7	117	5	HV3S_MOUSE IG HEAVY CHAIN V-III	3.66e-84
39	514	55.5	119	5	HV38_MOUSE IG HEAVY CHAIN V-III	9.86e-84
40	512	55.3	113	5	HV34_MOUSE IG HEAVY CHAIN V-III	2.66e-83
41	511	55.2	117	5	HV58_MOUSE IG HEAVY CHAIN V-III	4.36e-83
42	510	55.1	119	5	HV37_MOUSE IG HEAVY CHAIN V-III	7.16e-83
43	506	54.6	119	5	HV49_MOUSE IG HEAVY CHAIN V-III	5.20e-82
44	502	54.2	117	5	HV59_MOUSE IG HEAVY CHAIN V-III	3.77e-81
45	501	54.1	115	5	HV32_MOUSE IG HEAVY CHAIN V-III	6.18e-81

ALIGNMENTS

RESULT	1	STANDARD	PRT	122 AA.
ID	HV3G_HUMAN			
AC	P01768;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DE	IG HEAVY CHAIN V-III REGION (CAM).			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; PRIMATES			
PN	[1]			
PP	SEQUENCE			
FX	MEDLINE: 81013459			
FA	LEHMAN D.W., PUTNAM F.W.;			
FI	PROC. NATL. ACAD. SCI. U.S.A. 77:3230-3243(1980).			
CC	-1- THIS MU CHAIN WAS ISOLATED FROM THE PLASMA OF A PATIENT WITH			
CC	MACROGLOBULINEMIA			
DR	PIR; A02051; M3HUM.			
DP	HSSP; P01607; 2FGW			
KW	IMMUNOGLOBULIN V REGION.			
FT	MOD_RES			
FT	NON_TER			
SQ	SEQUENCE			
Query Match	76.6%	Score 700	DP 5	Length 122.
Best Local Similarity	69.6%	Pred. No. 2.75e-124		
Matches	87	Conservative 26	Mismatches 8	Indels 4
Gaps	3			
Db	1	qvelsgggvzpgzslrslscasgftfsnyamhwvrrppgkglewvavisybbbkyy	60	
Qy	1	EVALLSGGGVWQPGPSLPLSCAASGFTFSVGMHWVPAPGKGLEWVAG1WFGSSNQV	60	
Db	61	absvkrftisdbstbtlylgraslractatryycardpkygyra--f--nywqgql	117	
Qy	61	STSVKGFVTSFNSPNTPLFANNSTFEDTAVVYCATV--VLFGSIKGRYYLENWGGTL	119	
Db	118	vtvss 122		
Qy	120	vtvss 124		
RESULT	2	STANDARD	PRT	121 AA.
ID	HV3I_HUMAN			
AC	P01771;			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			

Thu Feb 26 07:06:09 1998

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DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (HIL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 79124695.
RA CHIU Y.-Y.H., LOPEZ DE CASTRO J.A., POLJAK R.J.;
RL BIOCHEMISTRY 18:553-580(1979).
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
DR PIR; A02054; G1HUHL.
DR HSP; P01607; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1
FT NON_TER 121
SQ SEQUENCE 121 AA; 13566 MW; 8E91B7EC CRC32;

Query Match 73.3%; Score 679; DB 5; Length 121;
Best Local Similarity 70.2%; Pred. No. 1.15e-119; Indels 3, Gaps 2;
Matches 87; Conservative 18; Mismatches 16;

Db 1 qvklvqagvgvqgrslrslscasgftsfygmhwrqapkgkglewvviyngsttyy 60
QY 1 EVOLLESGGVVQGRSLRSLSCASGFTFSAYGMHWRQAPKGKLEWVAGIFDGSNQY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 qdsvkrftisrdnskrtylmzmslrtdtavvycardp--dilta-fsfdywqgqlv 117
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 118 tvss 121
QY 121 TVSS 124

RESULT 3
ID HV3H_HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (GA).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 74175307.
RA FLORENT G., LEHMAN D., PUTNAM F.W.;
RL BIOCHEMISTRY 13:2482-2498(1974).
CC -!- THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN
DR PIR; A02052; M3HUGA.
DR HSP; P01772; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1
FT NON_TER 122
SQ SEQUENCE 122 AA; 13166 MW; D68R085E CRC32;

Query Match 73.0%; Score 676; DB 5; Length 122;
Best Local Similarity 63.2%; Pred. No. 5.23e-119; Indels 4, Gaps 2;
Matches 79; Conservative 33; Mismatches 9;

Db 1 qvzlvszsggavvqgrslrslscasgftsfygmhwrqapkgkglzslvisybgbbzyy 60
QY 1 EVOLLESGGVVQGRSLRSLSCASGFTFSAYGMHWRQAPKGKLEWVAGIFDGSNQY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 aasvkrftisrbbskbtmylenmlraentaavvycarsgialgsvaqtdy---wzqtl 117
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 118 tvss 122
QY 121 TVSS 124

RESULT 5
ID HV3H_HUMAN STANDARD; PRT; 119 AA.
AC P01770;

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RESULT 4
ID HV3K_HUMAN STANDARD; PRT; 126 AA.
AC P01772;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-MAR-1992 (REL. 21, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (KOL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE; 83289131.
RA SCHMIDT W.E., JUNG H.-D., PALM W., HILSCHMANN N.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 364:713-747(1983).
DR PIR; A02055; G1HUKL.
DR PDB; 2FB4; 12-JUL-89.
DR FDB; 2IG2; 12-JUL-89.
KW IMMUNOGLOBULIN V REGION; 3D-STRUCTURE.
FT MOD_RES 1
FT DISULFID 22
FT NON_TER 126
FT STRAND 3
FT STRAND 11
FT TURN 14
FT STRAND 18
FT TURN 25
FT HELIX 29
FT STRAND 31
FT TURN 41
FT STRAND 46
FT TURN 51
FT STRAND 53
FT TURN 58
FT STRAND 60
FT TURN 62
FT STRAND 68
FT TURN 74
FT STRAND 78
FT TURN 83
FT HELIX 88
FT STRAND 92
FT TURN 99
FT STRAND 106
FT TURN 107
FT STRAND 109
FT STRAND 113
FT STRAND 113
FT STRAND 120
FT STRAND 124
SQ SEQUENCE 126 AA; 13718 MW; 14F1E0F0 CRC32;

Query Match 72.2%; Score 669; DB 5; Length 126;
Best Local Similarity 71.4%; Pred. No. 1.80e-117; Indels 2; Gaps 2;
Matches 90; Conservative 17; Mismatches 17;

Db 1 qvqlvszsggavvqgrslrslscasgftsfygmhwrqapkgkglzslvisybgbbzyy 60
QY 1 EVOLLESGGVVQGRSLRSLSCASGFTFSAYGMHWRQAPKGKLEWVAGIFDGSNQY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 adsvkrftisrdnskrtylmzmslrtdtavvycardpavvycarsgialgsvaqtd 120
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 SDSVKGRFTVSRDNRSLRFLQMSLRPDTAVVYCA TEVLFGSIKGRYVLENWGQTL 118
QY 121 TVSS 126
QY 119 LTVSS 124

RESULT 5
ID HV3I_HUMAN STANDARD; PRT; 119 AA.
AC P01770;

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DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (NIE)
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA.
OC EUTHERIA, PRIMATES.
RN [1]
RP SEQUENCE. 77070269.
RX MEDLINE: 77070269.
RA FOSTLINGER H., HILSCHMANN N.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1571-1604(1976)
PN [2]
RX DISULFIDE BOND.
RX MEDLINE: 77070267.
RA DREXER L., SCHWARZ J., REICHEL W., HILSCHMANN N.;
FL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1515-1540(1976)
CC -!- THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA PROTEIN.
DR PIR: A02053; G1H0N1.
DR HSP: P01607; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID
FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA, 13242 MW, 57033A8E CRC32;

Query Match 68.7%; Score 636; DB 5; Length 119;
Best Local Similarity 68.5%; Pred. No. 3,09e-110;
Matches 85; Conservative 22; Mismatches 12; Indels 5; Gaps 4;

Db 1 qvqlvsggvvqpsrlscaasgftsfytlhwrtqapkglewvavmsygbkhy 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGVVQPSRLSCAASGFTSFAYGMHWVPQAPGKLEWVAVMSYGB 60

Db 61 adsvnrffisrdsntkntlylmnsrlpdtavyyca-ir-dtam--ff-ahwgqtlv 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRFTVSRDNSPNTLFLMNSLPEDTAVYVCATEVLFGSKRYYLENWSGQTLV 120

Db 116 tvss 119
|||||
QY 121 TVSS 124

RESULT 6
ID HV3E_HUMAN STANDARD: PRT: 119 AA.
AC P01773;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (BUR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA.
OC EUTHERIA, PRIMATES.
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE: 79151016.
RA PUTNAM F.W., LIU Y.-S.V., LOW T.L.K.;
RL J. BIOL. CHEM. 254:2865-2874(1979)
DR PIR: A02056; A1H0BR.
DR HSP: P01772; IFGV.
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT MOD_RES 1 1 PYROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT CARBOHYD 28 28
FT NON_TER 119 119
SQ SEQUENCE 119 AA, 12981 MW, 323A4FEL CRC32;

Query Match 65.9%; Score 610; DB 5; Length 119;
Best Local Similarity 65.0%; Pred. No. 1.4de-104;
Matches 80; Conservative 23; Mismatches 15; Indels 5; Gaps 2;

Db 1 qvqlvsggvvqpsrlscaasgftsfytlhwrtqapkglewvavmsygbkhy 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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QY 1 EVQLLESGGVVQPSRLSCAASGFTSFAYGMHWVPQAPGKLEWVAVMSYGB 60
Db 61 adsvnrffisrdsntkntlylmnsrlpdtavyyca-ir-dtam--ff-ahwgqtlv 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRFTVSRDNSPNTLFLMNSLPEDTAVYVCATEVLFGSKRYYLENWSGQTLV 120

Db 116 tvs 118
|||||
QY 121 TVS 123

RESULT 7
ID HV3E_HUMAN STANDARD: PRT: 117 AA.
AC P01764;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PREDNSOP V-III REGION (VH26).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA.
OC EUTHERIA, PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 81101090.
RA MATHYSENS G., RABBITTS T.H.;
FL PROC. NATL. ACAD. SCI. U.S.A. 77:6561-6565(1980).
DR EMBL: J08236; G553412; -.
DR EMBL: M35415; G553422; -.
DR PIR: A02047; H3HC26.
DR HSP: P01772; IFGM.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION (VH26)
FT NON_TER 117 117
SQ SEQUENCE 117 AA, 12582 MW, 15A21B2A CRC32;

Query Match 64.6%; Score 598; DB 5; Length 117;
Best Local Similarity 81.4%; Pred. No. 6.16e-102;
Matches 79; Conservative 12; Mismatches 6; Indels 0; Gaps 0;

Db 20 evqllesggvvqpsrlscaasgftsfytlhwrtqapkglewvavmsygbkhy 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGVVQPSRLSCAASGFTSFAYGMHWVPQAPGKLEWVAVMSYGB 60

Db 60 gdsvkgrftisrdsntkntlylmnsrlpdtavyyca 115
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRFTVSRDNSPNTLFLMNSLPEDTAVYVC 97

RESULT 8
ID HV3E_HUMAN STANDARD: PRT: 120 AA.
AC P01766;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (BRO).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA, METAZOA, CHORDATA, VERTEBRATA, TETRAPODA, MAMMALIA.
OC EUTHERIA, PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 77117574.
RA CAPRA J.D., HOPPER J.E.;
RL IMMUNOCHEMISTRY 13:996-999(1976).
CC -!- THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE SERUM OF A
PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM TYPE.
DR PIR: A02049; M3HUBW.
DR HSP: P01772; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT NON_TER 120 120
SQ SEQUENCE 120 AA, 13227 MW, B40C4FEL CRC32;

Query Match 64.0%; Score 593; DB 5; Length 120;

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QY 1 EVOLLESGGVQVQPSRLSLSCAASGFTFSAYGMHWWPQAPKGLWVAGIWDGSGNQY 60
 Db 77 advtkrftisrdnphkntflqmtslrsedtamyyca---wqny--pyyamdvwgsgts 131
 QY 61 SDSVKGFTVSRNSPNTLFIQMSLPPDTAVVYCAVEVLFSGIKGPIY-LENWQGGIL 119
 Db 132 vtvs 136
 QY 120 TVSS 124
 RESULT 12
 ID HV3M_HUMAN STANDARD: PRT: 119 AA.
 AC P01775;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN V-III REGION (LAY).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 75046755.
 RA CAPRA J.D., KEOHE J.M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:4032-4036(1974).
 CC -!- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 DR PIR; A02058; M3HUPM.
 DR HSSP; P01772; IIGV.
 KW IMMUNOGLOBULIN V REGION.
 FT NON_TER 119 119
 SQ SEQUENCE 119 AA; 12858 MW; 1CEG116C CRC32;

Query Match 62.1%; Score 575; DB 5; Length 119;
 Best Local Similarity 63.9%; Pred. No. 6 23e-q7;
 Matches 78; Conservative 25; Mismatches 13; Indels 6; Gaps 4.
 Db 2 vqllesggglvqpgsrlscaasgftfsasamsvwrqapkgglewva--wkyengndkh 59
 QY 2 VQLESQGVQVQPSRLSLSCAASGFTFSAYGMHWWPQAPKGLWVAGIWF-DSNQY 59
 Db 60 yadsvngfrftisrdnphkntflqmgldqzvsalyycarda--qpyvsptffahwggtl 117
 QY 60 YDSVKGFTVSRNSPNTLFIQMSLPPDTAVVYCAVEVLFSGIKGPIY-LENWQGGIL 119
 Db 118 vt 119
 QY 120 VT 121

RESULT 13
 ID HV3T_HUMAN STANDARD: PRT: 116 AA.
 AC P01781;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN V-III REGION (GAL).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 75059123.
 RA WATANABE S., BARNIKOL H.U., HORN J., BERTRAM T., HILSCHMANN N.;
 RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 354:1505-1509(1973).
 RN [2]
 RP REVISION TO THE COMPOSITION OF 28-33.
 RA HILSCHMANN N.;
 RL SUBMITTED (JUN-1975) TO THE PIR DATA BANK.
 CC -!- THIS MJ CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN
 DR PIR; A02064; M3HUGL.
 DR HSSP; P01607; IFGV.

KW IMMUNOGLOBULIN V REGION.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12730 MW; F112826C CRC32;
 Query Match 61.6%; Score 570; DB 5; Length 116;
 Best Local Similarity 70.2%; Pred. No. 7 60e-96;
 Matches 87; Conservative 14; Mismatches 15; Indels 8; Gaps 3;
 Db 1 exqlvesggdlvqpgsrlscaasgfbfblgtwrrqapkgglewvanik-bgszby 60
 QY 1 EVOLLESGGVQVQPSRLSLSCAASGFTFSAYGMHWWPQAPKGLWVAGIWFDSNQY 60
 Db 61 vdsvkgrftisrdnphkntflqmslrsedtamyyca---wgy---gdy---wqsgtlv 112
 QY 61 SDSVKGFTVSRNSPNTLFIQMSLPPDTAVVYCAVEVLFSGIKGPIY-LENWQGGIL 120
 Db 113 tvst 116
 QY 121 TVSS 124
 RESULT 14
 ID HV3M_HUMAN STANDARD: PRT: 119 AA.
 AC P01774;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN V-III REGION (POM).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 75046755.
 RA CAPRA J.D., KEOHE J.M.;
 RL PROC. NATL. ACAD. SCI. U.S.A. 71:4032-4036(1974).
 CC -!- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 DR PIR; A02057; M3HUPM.
 DR HSSP; P01772; IFGV.
 KW IMMUNOGLOBULIN V REGION.
 FT VARIANT 54 54 N -> D (POSSIBLY DUE TO DEAMINATION
 FT NON_TER 119 119 DURING ISOLATION).
 SQ SEQUENCE 119 AA; 12953 MW; 2A5697C2 CRC32;
 Query Match 60.8%; Score 563; DB 5; Length 119;
 Best Local Similarity 63.4%; Pred. No. 2 51e-94;
 Matches 78; Conservative 25; Mismatches 14; Indels 6; Gaps 4.
 Db 1 evqllesggglvqpgsrlscaasgftfsasamsvwrqapkgglewva--wkyengndk 58
 QY 1 EVOLLESGGVQVQPSRLSLSCAASGFTFSAYGMHWWPQAPKGLWVAGIWF-DSNQ 58
 Db 59 hyadsvngfrftisrdnphkntflqmslrsedtamyyca---qpyvsptffahwggtl 116
 QY 59 YDSVKGFTVSRNSPNTLFIQMSLPPDTAVVYCAVEVLFSGIKGPIY-LENWQGGI 118
 Db 117 lvt 119
 QY 119 LVT 121
 RESULT 15
 ID HV3E_HUMAN STANDARD: PRT: 115 AA.
 AC P01767;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DE IG HEAVY CHAIN V-III REGION (BUT).
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.

US-08-844-215-5.rsp

Thu Feb 26 07:06:09 1998

```

RN  SEQUENCE.
RP  MEDLINE: 78137069.
RX  TORANO A.; PUTNAM F.W.;
RA  PROC. NATL. ACAD. SCI. U.S.A. 75:966-969(1978).
FL  PROC. NATL. ACAD. SCI. U.S.A. 75:966-969(1978).
CC  -!- THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C REGION OF THIS
CC  MYELOMA PROTEIN IS ALSO GIVEN.
DR  PIR: A02050; A2HUBU.
DR  HSP: P01772; IFGV.
DR  IMMUNOGLOBULIN V REGION.
KW  NON_TER 115 115
FT  SEQUENCE 115 AA: 12379 MW: 90803472 CRC32:
SQ

Query Match 59.8%; Score 554; DB 5; Length 115;
Best Local Similarity 69.0%; Pred. No. 2.25e-92; Indels 1; Gaps 1;
Matches 69; Conservative 21; Mismatches 9;

Db 1 evqlvetgggllqpggslrlscaasgftvshmswvraqpgkalzwsai-yrgqttty 59
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 EVQLLESGGAVQPGRLSLRLSCAASGFTFSAYGMHWRQAPCKGLEWVAGIWDGSNQYY 60
   |||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 adsvkgrftisrddsbvtvylgmbslraedtaavyycardl 99
   :|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 SDSVKGRFTVSRDNRNRTLEFQMSLRPEDTAVYTCATEV 100
   :|||||:||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Search completed: Tue Feb 24 07:11:14 1998
 Job time : 10 secs.

M E R E H
(TW)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run On: Tue Feb 24 07:11:22 1998; MasPar time 8.34 Seconds
Tabular output not generated. 452,970 Million cell updates/sec

Title: >US-08-844-215-5
Description: (1-124) from US08844215.paf
Perfect Score: 926
Sequence: 1 EVQILFSGGGVWVQPSRLPLIKGRVYLENWGGTLIVSS 124

Scoring table: PAM 150
Gap 11

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0*
Listing first 45 summaries

Database: pir53
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann11 16:unann12 17:unann13
18:unrev

Statistics: Mean 41.610; Variance 126.095; scale 0.330
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DB ID	Description
1	746	80.6	122 7 S31117	Ig heavy chain - hum 1.10e-81
2	720	77.8	121 7 S19666	Ig heavy chain V reg 3.73e-78
3	719	77.6	138 7 S48797	Ig heavy chain V reg 5.10e-78
4	713	77.0	133 7 A49028	Ig heavy chain V-III 3.32e-77
5	704	76.0	132 7 E36005	Ig heavy chain V reg 5.51e-76
6	703	75.9	133 7 S31503	Ig heavy chain V reg 7.53e-75
7	700	75.6	132 2 M3H2M	Ig heavy chain V-III 4.92e-75
8	696	75.2	134 7 S31574	Ig heavy chain V reg 6.58e-75
9	695	75.1	120 7 S31112	Ig heavy chain - hum 9.12e-75
10	693	74.8	118 7 S31116	Ig heavy chain - hum 1.70e-74
11	689	74.5	120 7 S36278	Ig heavy chain V reg 4.33e-74
12	689	74.4	133 7 S69310	Ig V-D-2 V-reg (KP) 5.92e-73
13	688	74.3	121 7 G36005	Ig heavy chain V reg 8.08e-74
14	688	74.3	135 7 S31598	Ig heavy chain V reg 8.08e-74
15	686	74.1	133 7 S31510	Ig heavy chain - hum 1.51e-73
16	584	73.9	121 7 S31104	Ig heavy chain (Subc 2.81e-72
17	694	73.9	160 7 S05271	Ig heavy chain precu 2.81e-73
18	683	73.8	119 7 S31111	Ig heavy chain - hum 3.84e-73
19	683	73.8	151 7 A60943	Ig heavy chain precu 3.84e-73
20	679	73.3	131 2 C:HPHL	Ig heavy chain V-III 1.33e-72

21 677 73.1 123 7 S31114 Ig heavy chain - hum 2.49e-72
22 676 73.0 122 2 M3H2M Ig heavy chain V-III 3.39e-72
23 674 72.8 119 7 S36005 Ig heavy chain V reg 6.32e-72
24 673 72.7 98 7 S26993 Ig heavy chain V reg 8.63e-72
25 673 72.7 123 7 S39493 Ig heavy chain - hum 8.63e-72
26 670 72.4 111 7 PH1642 Ig heavy chain V reg 2.19e-71
27 669 72.3 126 2 G1HUKL Ig heavy chain V-III 3.00e-71
28 668 72.1 124 7 S20782 Ig heavy chain V reg 4.09e-71
29 668 72.1 130 7 S31501 Ig heavy chain V reg 4.09e-71
30 663 71.6 119 7 S37453 Ig mu chain - human 1.94e-70
31 663 71.6 120 7 S44111 Ig heavy chain V-D-J 1.94e-70
32 662 71.5 137 7 S31701 Ig heavy chain V reg 2.64e-70
33 662 71.5 140 7 S31588 Ig heavy chain V reg 2.64e-70
34 659 71.2 117 7 S36269 Ig heavy chain V reg 6.71e-70
35 659 71.2 125 7 S37455 Ig mu chain - human 9.15e-70
36 658 71.1 113 7 S38490 Ig heavy chain V reg 1.25e-69
37 657 71.0 120 7 S36273 Ig heavy chain - hum 1.25e-69
38 657 71.0 122 7 S31119 Ig heavy chain V reg 1.70e-69
39 656 70.8 119 7 S31107 Ig heavy chain - hum 1.70e-69
40 655 70.7 123 7 S30532 Ig heavy chain V reg 2.33e-69
41 655 70.7 140 7 S31586 Ig heavy chain V reg 2.33e-69
42 653 70.5 120 7 S48798 Ig heavy chain V reg 4.33e-69
43 653 70.5 121 7 I55673 IGM - human (fragmen 4.33e-69
44 653 70.5 134 7 S31579 Ig heavy chain V reg 4.33e-69
45 652 70.4 114 7 S46290 Ig heavy chain V reg 5.90e-69

ALIGNMENTS

RESULT 1
ENTRY S31117 #type complete
TITLE Ig heavy chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 16-Aug-1996
ACCESSIONS S31117
REFERENCE S31104
#authors Rappaport, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman, P.K.B
#journal Exp. J. Immunol. (1992) 22:247-251
#title Restricted utilization of germ-line V(H)3 genes and short diverse third complementarity-determining regions (CDR3) in human fetal B lymphocyte immunoglobulin heavy chain rearrangements.
#accession S31117
#status preliminary; nucleic acid sequence not shown;
#molecule_type mRNA
#residues 1-122 #label RAA
#cross-references EMBL:X62967
#note the nucleotide sequence was submitted to the EMBL Data Library, October 1991
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE #domain immunoglobulin homology #label IMM
15-98
SUMMARY #length 122 #molecular_weight 13664 #checksum 8338
Query Match 90.6%; Score 746; DB 7; Length 122;
Best Local Similarity 73.0%; Pred. No. 1.10e-81;
Matches 98; Conservative 17; Mismatches 7; Gaps 2;
Db 1 qvqlvesggvwpqprslrlscasagftfssygmhwrqspkqlgwaviwvsgnky 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVQILFSGGGVWVQPSRLPLSCAASGFTFSSAYDMHWPAPAKSKLEWVASINFDGSGNQY 50
Db 61 adsvkgfttsrdnsknltlylqmnslraetavyyccard-ffgppn-wshfdywggttlv 118
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKGFTVSPONSRLTLFLQMSLPPEETAVYYCAIEVIFSSIKGRVYLENWGGTLV 120
Db 119 tyss 122
:|||||
QY 121 TVSE 124

```

RESULT      2
ENTRY       S19666      #type complete
TITLE       Ig heavy chain V region (VH3DJH4) - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change
              16-Aug-1996

ACCESSIONS  S19666
REFERENCE    S19663
#authors     Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.;
              Griffiths, A.D.; Winter, G.
#journal     J. Mol. Biol. (1991) 222:581-597
#title       By-passing immunization: Human antibodies from V-gene
              libraries displayed on phage.
#cross-references MUID:92085276
#accession    S19666
#molecule_type mRNA
#residues     1-121 ##label MAP
#cross-references EMBL:X61646
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE       #domain immunoglobulin homology #label IMM
              #length 121 #molecular-weight 13296 #checksum 9195
              15-98
SUMMARY
Query Match 77.8%; Score 720; DB 7; Length 121;
Best Local Similarity 79.0%; Pred. No. 3,73e-78;
Matches 98; Conservative 14; Mismatches 9; Indels 3; Gaps 3;

Db 1 qvqlvesgqgvvqprsrllscasqgftfssygmhwvraqpdkglewvavisdysnky 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGQVQPGKRSRLSCASGFTFSAYGMHWVRAQPGKLEWVAVIGDGSNQYY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 adsvkgrftisrdnsknltlylqmslraedtavyycaetg-vysgwg-yf-dywgqgtlv 117
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRFTVSRDNRSLTFLQMSLRPEDTAVYYCATEVLFSGIKGRYILENNGWGQTLV 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 118 tvss 121
   ||||
QY 121 TVSS 124

RESULT      3
ENTRY       S48797      #type complete
TITLE       Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
              16-Aug-1996

ACCESSIONS  S48797
REFERENCE    S48797
#authors     Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
#submission submitted to the EMBL Data Library, October 1994
#description Molecular characterization of natural human anti-Sm
              autoantibodies.
#accession    S48797
#status       preliminary
#molecule_type mRNA
#residues     1-128 ##label MAP
#cross-references EMBL:246379
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS      heterotetramer; immunoglobulin
FEATURE       #domain immunoglobulin homology #label IMM
              #length 128 #molecular-weight 14474 #checksum 9058
              15-98
SUMMARY
Query Match 77.6%; Score 719; DB 7; Length 128;
Best Local Similarity 77.3%; Pred. No. 5.10e-78;
Matches 99; Conservative 13; Mismatches 12; Indels 4; Gaps 1;

Db 1 qvqlvesgqgvvqprsrllscasqgftfssygmhwvraqpdkglewvavisdysnky 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGQVQPGKRSRLSCASGFTFSAYGMHWVRAQPGKLEWVAVIGDGSNQYY 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 61 adsvkgrftisrdnsknltlylqmslraedtavyycaetg-vysgwg-yf-dywgqgtlv 119
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGRFTVSRDNRSLTFLQMSLRPEDTAVYYCATEVLFSGIKGRYILENNGWGQTLV 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 120 tvss 123
   ||||
QY 121 TVSS 124

RESULT      5
ENTRY       E36005      #type complete
TITLE       Ig heavy chain V region (M72) - human
ORGANISM    #formal_name Homo sapiens #common_name man
DATE        21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
              16-Aug-1996

ACCESSIONS  E36005
REFERENCE    A36005
#authors     Schroeder Jr., H.W.; Wang, J.Y.
#journal     Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150
#title       Preferential utilization of conserved immunoglobulin heavy
              chain variable gene segments during human fetal life.
#cross-references MUID:90349571
#accession    E36005
#status       preliminary
#molecule_type mRNA
#residues     1-122 ##label SCH

```

```

##cross-references GB:M34030
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY #length 122 #molecular_weight 13527 #checks 630

Query Match 76.3%; Score 703; DB 7; Length 122;
Best Local Similarity 77.8%; Pred. No. 7.53e-76;
Matches 99; Conservative 13; Mismatches 5; Indels 7; Gaps 2;

Db 16 qvlgvsgggvvpqgrslrlscasgftfssygmhwrqapqgkglewvavisdgskyy 75
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVQLLESGGVVQPGRLSRUSCAASGFTFSAYGMHWRQAPQKGLWVAVIGFDGSKYY 60

Db 61 adsvkgftisrdnksntlylqmslraedavvycaakd-iff-nywaggtlv 128
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SDSVKGRFTVSRGNSPNTFLQWNSLRPEPTAVVYCAITEVFGSIK3FYYLENWQ2TLV 120

Db 129 tvss 132
QY :|||||:
121 TVSS 124

RESULT 7
ENTRY M3HUM #type complete
TITLE Ig heavy chain V-III region (Cam) - human
OPORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Aug-1980 #sequence_revision 23-Oct-1981 #text_change
31-Mar-1997
ACCESSIONS A02051
REFERENCE A02051

##cross-references GB:M34030
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY #length 122 #molecular_weight 13527 #checks 630

Query Match 76.3%; Score 704; DB 7; Length 122;
Best Local Similarity 77.6%; Pred. No. 5.51e-76;
Matches 97; Conservative 15; Mismatches 8; Indels 4; Gaps 3;

Db 1 qvlgvsgggvvpqgrslrlscasgftfssygmhwrqapqgkglewvavisdgskyy 60
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVQLLESGGVVQPGRLSRUSCAASGFTFSAYGMHWRQAPQKGLWVAVIGFDGSKYY 60

Db 61 adsvkgftisrdnksntlylqmslraedavvycaakd-hss--swygmndvwaqgtt 117
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SDSVKGRFTVSRGNSPNTFLQWNSLRPEPTAVVYCAITEVFGSIK3FYYLENWQ2JTL 119

Db 118 tvss 122
QY :|||||:
120 TVSS 124

RESULT 6
ENTRY S31603 #type complete
TITLE Ig heavy chain V region - human
OPORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change
16-Aug-1996
ACCESSIONS S31603
REFERENCE S31585
AUTHORS Cuisinier, A.M.; Gauthier, L.; Boubili, L.; Fougereau, M.;
Tonnelie, C.
SUBMISSION submitted to the EMBL Data Library, June 1992
DESCRIPTION Mechanisms that generate human immunoglobulin diversity
operate from the 8th week of gestation in fetal liver.
ACCESSION S31603
STATUS preliminary
#molecule_type mRNA
#residues 1-132 #label CUI
##cross-references EMBL:Z14168
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
30-113 #domain immunoglobulin homology #label IMM
SUMMARY #length 132 #molecular_weight 14696 #checks 8700

Query Match 75.9%; Score 703; DB 7; Length 132;
Best Local Similarity 79.8%; Pred. No. 7.53e-76;
Matches 99; Conservative 13; Mismatches 5; Indels 7; Gaps 2;

Db 16 qvlgvsgggvvpqgrslrlscasgftfssygmhwrqapqgkglewvavisdgskyy 75
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVQLLESGGVVQPGRLSRUSCAASGFTFSAYGMHWRQAPQKGLWVAVIGFDGSKYY 60

Db 76 adsvkgftisrdnksntlylqmslraedavvycaakd-iff-nywaggtlv 128
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SDSVKGRFTVSRGNSPNTFLQWNSLRPEPTAVVYCAITEVFGSIK3FYYLENWQ2TLV 120

Db 129 tvss 132
QY :|||||:
121 TVSS 124

RESULT 7
ENTRY M3HUM #type complete
TITLE Ig heavy chain V-III region (Cam) - human
OPORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Aug-1980 #sequence_revision 23-Oct-1981 #text_change
31-Mar-1997
ACCESSIONS A02051
REFERENCE A02051

```

```

#authors Lehman, D.W.; Putnam, F.W.
#journal Proc. Natl. Acad. Sci. U.S.A. (1980) 77:3239-3243
#title Amino acid sequence of the variable region of a human mu
chain: location of a possible J-H segment.
#cross-references MUID:81013859
#accession A02051
##molecule_type protein
##residues 1-122 #label LEH
COMMENT This mu chain was isolated from the plasma of a patient with
macroglubulinemia.
GENETICS
#gene GDB:IGHV@
#cross-references QDB:128528
#map_position 1432.33-1432.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin; pyroglutamic acid
FEATURE
15-98 #domain immunoglobulin homology #label IMM
1 #modified site pyroglutamic acid (Gln) #status
experimental
22-96 #disulfide_bonds #status predicted
SUMMARY #length 122 #molecular_weight 13668 #checks 7281

Query Match 75.6%; Score 700; DB 2; Length 122;
Best Local Similarity 69.6%; Pred. No. 1.92e-75;
Matches 87; Conservative 26; Mismatches 8; Indels 4; Gaps 3;

Db 1 qvlgvsgggvvpqgrslrlscasgftfssygmhwrqapqgkglewvavisdgskyy 60
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVQLLESGGVVQPGRLSRUSCAASGFTFSAYGMHWRQAPQKGLWVAVIGFDGSKYY 50

Db 61 adsvkgftisrdnksntlylqmslraedavvycaakd-lygbyra--f-nywaggtlv 117
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SDSVKGRFTVSRGNSPNTFLQWNSLRPEPTAVVYCAITEVFGSIK3FYYLENWQ2JTL 119

Db 118 tvss 122
QY :|||||:
120 TVSS 124

RESULT 8
ENTRY S31674 #type fragment
TITLE Ig heavy chain V region - human (fragment)
OPORGANISM #formal_name Homo sapiens #common_name man
DATE 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
16-Aug-1996
ACCESSIONS S31674
REFERENCE S31585
AUTHORS Cuisinier, A.M.; Gauthier, L.; Boubili, L.; Fougereau, M.;
Tonnelie, C.
SUBMISSION submitted to the EMBL Data Library, June 1993
DESCRIPTION Mechanisms that generate human immunoglobulin diversity
operate from the 8th week of gestation in fetal liver.
ACCESSION S31674
STATUS preliminary
#molecule_type mRNA
#residues 1-139 #label CUI
#cross-references EMBL:Z14204
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
34-117 #domain immunoglobulin homology #label IMM
SUMMARY #length 139 #checks 3756

Query Match 75.2%; Score 696; DB 7; Length 139;
Best Local Similarity 78.2%; Pred. No. 6.68e-75;
Matches 97; Conservative 14; Mismatches 9; Indels 4; Gaps 3;

Db 20 qvlgvsgggvvpqgrslrlscasgftfssygmhwrqapqgkglewvavisdgskyy 79
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVQLLESGGVVQPGRLSRUSCAASGFTFSAYGMHWRQAPQKGLWVAVIGFDGSKYY 60

Db 80 adsvkgftisrdnksntlylqmslraedavvycaakd-fff-wf--dpwaggtlv 135

```

US-08-844-215-5.rpr

Thu Feb 26 07:06:08 1998

```

##residues 1-118 ##label RAA
##cross-references EMBL:X62966
##note the nucleotide sequence was submitted to the EMBL Data
Library, October 1991
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 118 #molecular-weight 12778 #checksum 4374

Query Match 74.8%; Score 693; DB 7; Length 118;
Best Local Similarity 79.0%; Pred. No. 1.70e-74;
Matches 98; Conservative 15; Mismatches 5; Indels 6; Gaps 3;

Db 1 qvqlvesggvvqpgrslrlscasgfftsygmhvrqgpkglewvavisydgsnkyy 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVOLLESGGGVVGPGRLSLSCAASGFTFSAYGMHVRQAPGKLEWVAGIWFEDGSNOYY 60
QY

Db 61 adsvkgrftisrdnsnkntlylqmnsrlraedtavvyatdy---wgagtlv 114
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SDSVKGRTFVSRDNRNLTFLQMSLRPEDTAVVYCATVFLFGSIKGRYYLENWGGQGLTV 120
QY

Db 115 tvss 118
|||||
QY 121 TVSS 124

RESULT 11
ENTRY S36278 #type fragment
TITLE Ig heavy chain V region (clone alpha-THY-23) - human
(fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996
ACCESSIONS S36278
REFERENCE S36256
AUTHORS Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
Embleton, M.J.; McCafferty, J.; Baier, M.; Hoiliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
G.
#journal EMBO J. (1993) 12:725-734
#title Human anti-self antibodies with high specificity from phage
display libraries.
#accession S36278
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-120 #label GRI
#cross-references EMBL:Z18830
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 120 #checksum 7337

Query Match 74.5%; Score 690; DB 7; Length 120;
Best Local Similarity 73.2%; Pred. No. 4.33e-74;
Matches 90; Conservative 18; Mismatches 12; Indels 3; Gaps 3;

Db 1 qvqlvesggvvqpgrslrlscasgfftsygmhvrqgpkglewvavisydgsnkyy 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVOLLESGGGVVGPGRLSLSCAASGFTFSAYGMHVRQAPGKLEWVAGIWFEDGSNOYY 60
QY

Db 61 adsvkgrftisrdnsnkntlylqmnsrlraedtavvyatdy---wgagtlv 117
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 SDSVKGRTFVSRDNRNLTFLQMSLRPEDTAVVYCATVFLFGSIKGRYYLENWGGQGLTV 120
QY

Db 118 tvs 120
|||||
QY 121 TVS 123

RESULT 12
ENTRY S69910 #type complete

```

```

TITLE      Ig V-D-J region (KR) - human
ORGANISM   #formal_name Homo sapiens #common_name man
DATE       14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change
          09-May-1997
ACCESSIONS S69910
REFERENCE   Sahota, S.; Hamblin, T.; Osier, D.G.; Stevenson, F.K.
#authors   Leukemia (1994) 8:1285-1289
#journal   Assessment of the role of clonogenic B lymphocytes in the
#title     pathogenesis of multiple myeloma.
#accession S69910
##status   preliminary: nucleic acid sequence not shown
##molecule_type mRNA
##residues 1-122 ##label SAH
##cross-references EMBL:Z33400
##note     the sequence of residues 108-122 and the corresponding
           nucleic acid sequence are not shown
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
SUMMARY       #length 122 #molecular-weight 13511 #checksum 583

Query Match      74.4%; Score 689; DB 7; Length 122;
Best Local Similarity 75.2%; Pred. No. 5.92e-74;
Matches 94; Conservative 15; Mismatches 12; Indels 4; Gaps 4;

Db 1 qvqlvesggvqpqsrllscasgftssygmhvwraqpdkglwlravysdgsnkyy 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGVPQPGPSLPFLCAASGFTFSAYGMHWPAPCKGKLEWAGWFDGSNYY 60

Db 61 adsvkrftisrdsnkntlylgmnsiraedtavvycaedrkw--gwalfdywgqgtlv 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKGPFTVSPKNSNTLFLMNSLPPTTAVVYCA-TEVLFSGIKRPFYILENMGQGTIL 119

Db 118 vtvs 122
   |||||
QY 120 vtvs 124

RESULT 13
ENTRY     G36005 #type complete
TITLE     Ig heavy chain V region (M74) - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
          16-Aug-1996
ACCESSIONS G36005
REFERENCE   Schroeder Jr., H.W.; Wang, J.Y.
#authors   Proc Natl Acad Sci U S A (1990) 87:6146-6150
#journal   Preferential utilization of conserved immunoglobulin heavy
#title     chain variable gene segments during human fetal life.
#cross-references MIM:90344571
#accession G36005
##status   preliminary
##molecule_type mRNA
##residues 1-121 ##label SCH
##cross-references GB:M34031
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS     heterotetramer; immunoglobulin
FEATURE      15-98
SUMMARY      #domain immunoglobulin homology #label IMM
           #length 121 #molecular-weight 13508 #checksum 6962

Query Match      74.3%; Score 688; DB 7; Length 121;
Best Local Similarity 77.4%; Pred. No. 8.08e-74;
Matches 96; Conservative 14; Mismatches 11; Indels 2; Gaps 2;

Db 1 qvqlvesggvqpqsrllscasgftssygmhvwraqpdkglwlravysdgsnkyy 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVQLLESGGVPQPGPSLPFLCAASGFTFSAYGMHWPAPCKGKLEWAGWFDGSNYY 60

Db 61 adsvkrftisrdsnkntlylgmnsiraedtavvycaedrkw--gwalfdywgqgtlv 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKGPFTVSPKNSNTLFLMNSLPPTTAVVYCA-TEVLFSGIKRPFYILENMGQGTIL 120

```

```

Db 118 tvss 121
   |||||
QY 121 tvss 124

RESULT 14
ENTRY     S31598 #type complete
TITLE     Ig heavy chain V region - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
          16-Aug-1996
ACCESSIONS S31598
REFERENCE   Collier, A.M.; Gauthier, L.; Boulik, L.; Fougereau, M.;
#authors   Tonnelie, C.
#submission submitted to the EMBL Data Library, June 1992
#description Mechanisms that generate human immunoglobulin diversity
           operate from the 8th week of gestation in fetal liver
#accession S31598
##status   preliminary
##molecule_type mRNA
##residues 1-135 ##label CUI
##cross-references EMBL:Z14170
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS     heterotetramer; immunoglobulin
FEATURE      31-114
SUMMARY      #domain immunoglobulin homology #label IMM
           #length 135 #molecular-weight 14957 #checksum 4425

Query Match      74.3%; Score 688; DB 7; Length 135;
Best Local Similarity 77.4%; Pred. No. 8.08e-74;
Matches 96; Conservative 15; Mismatches 8; Indels 5; Gaps 4;

Db 17 qvqlvesggvqpqsrllscasgftssygmhvwraqpdkglwlravysdgsnkyy 76
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVQLLESGGVPQPGPSLPFLCAASGFTFSAYGMHWPAPCKGKLEWAGWFDGSNYY 60

Db 77 adsvkrftisrdsnkntlylgmnsiraedtavvycaedrkw--gwalfdywgqgtlv 131
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 SDSVKGPFTVSPKNSNTLFLMNSLPPTTAVVYCA-TEVLFSGIKRPFYILENMGQGTIL 120

Db 132 tvss 135
   |||||
QY 121 tvss 124

RESULT 15
ENTRY     S31510 #type complete
TITLE     Ig heavy chain - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
          16-Aug-1996
ACCESSIONS S31510
REFERENCE   Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
#authors   submitted to the EMBL Data Library, December 1992
#description Dominance of clonotypic patterns and variable gene usage of
           anti-DNA autoantibodies from patient with lupus.
#accession S31510
##status   preliminary
##molecule_type mRNA
##residues 1-133 ##label CHA
##cross-references EMBL:X69865
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS     heterotetramer; immunoglobulin
FEATURE      25-109
SUMMARY      #domain immunoglobulin homology #label IMM
           #length 133 #molecular-weight 14779 #checksum 9812

Query Match      74.1%; Score 686; DB 7; Length 133;
Best Local Similarity 76.4%; Pred. No. 1.51e-73;
Matches 94; Conservative 17; Mismatches 10; Indels 2; Gaps 2;

```

US-08-844-215-5.rpr

Thu Feb 26 07:06:08 1998

Db 13 vhlvesggvvpqarslriscasqftfssfamhwrqapkglewaaaisydsneyya 72
QY 2 VOLLESGGVVPGESLRLSCAASGTFPSAYGMHWRQAPKGLEWVAGIWFDSNQYYS 61
Db 73 dsvkgrftvsrdnskntlylgmnsraedtavyyicar-vsreaf-vriaftywqhtllt 130
QY 62 DSVKGRFTVSRDNRNTLFLQMNLSLRPDTAVYYCATEVLFSGIKGRYILENMGQGTLYT 121
Db 131 vss 133
QY 122 VSS 124

Search completed: Tue Feb 24 07:12:14 1998
Job time : 42 secs.

W O E R E H
***** (TM)

Release 2 ID John F. Collins, Biocomputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:30:15 1998. Master time 3:55:30.00
Tabular output not generated. 177,836 Million cell updates/sec

Title: >US-08-844-215-5
Description: (1-124) from US08844215.pep
Perfect Score: 926
Sequence: 1 EVOLLESGGVVQPGSLRL... IKPYYLENWGGTLTVSS 124

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:58 10:59
10:PT92 11:PT93 12:PT94 13:PT95 14:PT96

Statistics: Mean 28.178 Variance 148.297 scale 0.190

Pred No is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	695	75.1	119	7	US-08-331- Sequence 45, Applicati	1.07e-45
2	687	74.2	125	7	US-08-478- Sequence 99, Applicati	4.64e-45
3	684	73.9	120	7	US-07-942- Sequence 35, Applicati	8.05e-45
4	683	73.8	141	6	US-08-259- Sequence 2, Applicatio	9.67e-45
5	683	73.8	141	7	US-08-468- Sequence 2, Applicatio	9.67e-45
6	682	73.7	125	11	PCT-US93-1 Sequence 1, Applicati	1.16e-44
7	674	72.8	125	11	PCT-US93-0 Sequence 43, Applicati	5.05e-44
8	672	72.6	122	11	PCT-US93-0 Sequence 14, Applicati	7.29e-44
9	670	72.4	122	11	PCT-US93-0 Sequence 12, Applicati	1.05e-43
10	660	71.3	125	7	US-07-942- Sequence 33, Applicati	6.59e-43
11	660	71.3	142	7	US-08-105- Sequence 2, Applicatio	6.59e-43
12	658	71.1	122	11	PCT-US93-0 Sequence 21, Applicati	9.51e-43
13	657	71.0	123	7	US-08-478- Sequence 94, Applicati	1.14e-42
14	655	70.7	116	6	US-08-211- Sequence 141, Applicati	1.65e-42
15	654	70.6	125	11	PCT-US93-1 Sequence 6, Applicatio	1.98e-42
16	654	70.6	125	11	PCT-US93-1 Sequence 5, Applicatio	1.98e-42
17	646	69.8	98	6	US-08-211- Sequence 118, Applicati	9.55e-42
18	640	69.1	117	7	US-07-942- Sequence 93, Applicati	2.58e-41
19	640	69.1	130	7	US-08-478- Sequence 93, Applicati	2.58e-41
20	640	69.1	130	7	US-08-478- Sequence 70, Applicati	2.58e-41
21	637	68.8	119	12	PCT-US94-0 Sequence 6, Applicati	4.47e-41
22	637	68.8	125	13	PCT-US95-0 Sequence 72, Applicati	4.47e-41

CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US 07/943,245
CC FILING DATE: 09 SEP-1992
CC CLASSIFICATION: 530
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (202) 292-7060
CC TELEFAX: (202) 293-7860
CC TELEX: 6491103
CC INFORMATION FOR SEQ ID NO: 35:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 120 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE 120 AA, 13421 MW, 78517 CN.

Query Match 73.9%; Score 684; DB 7; Length 120;
Best Local Similarity 77.2%; Pred. No 8,05e-45;
Matches 95; Conservative 14; Mismatches 11; Indels 3; Gaps 2;

Db 1 QVQLVESGGGVVQPGPSLPLSQAASGFTFSVAMHWVQAPKSLKLEWAVSYVDSNKKY 60
QY 1 EVQLLESQGVVQPGPSLPLSQAASGFTFSVAMHWVQAPKSLKLEWAVSYVDSNKKY 60
Db 61 ADSVKGPFITSDNSKNTLYLQMSLRAEDTAVYYCAPDRK-DW--GMAIFDYWGQGLV 117
QY 61 SDSVKGPFITSDNSKNTLYLQMSLRAEDTAVYYCAPDRK-DW--GMAIFDYWGQGLV 120
Db 118 TVS 120
QY 121 TVS 123

RESULT 4
ID US-08-259-372A-2 STANDARD: PPT: 141 AA
XX xxxxxx
XX 01-JAN-1900
XX Sequence 2, Application US/08259372A
XX Sequence 2, Application US/08259372A
XX Patent No. 5565354
XX GENERAL INFORMATION:
XX APPLICANT: Ostberg, Lars G.
XX TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
XX TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIG
EN
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1 0, Version #1 30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/259,372A
CC FILING DATE: 14-JUN-1994
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/871,426
CC FILING DATE: 21-APR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/870,036
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: US 07/538,796
CC FILING DATE: 15-MAY-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/192,754
CC FILING DATE: 11-MAY-1988
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/925,196
CC FILING DATE: 31-OCT-1996
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 06/904,517
CC FILING DATE: 05-SEP-1986
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-50-7
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 328-2400
CC TELEFAX: (415) 576-0300
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 141 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 141 AA, 15613 MW, 114738 CN;

Query Match 73.8%; Score 683; DB 6; Length 141;
Best Local Similarity 77.6%; Pred. No 9,67e-45;
Matches 97; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

Db 20 QVQLVESGGGVVQPGPSLPLSQAASGFTFSVAMHWVQAPKSLKLEWAVSYVDSNKKY 79
QY 1 EVQLLESQGVVQPGPSLPLSQAASGFTFSVAMHWVQAPKSLKLEWAVSYVDSNKKY 60
Db 80 ADSVKGPFITSDNSKNTLYLQMSLRAEDTAVYYCAPDRK-DW--GMAIFDYWGQGLV 136
QY 61 SDSVKGPFITSDNSKNTLYLQMSLRAEDTAVYYCAPDRK-DW--GMAIFDYWGQGLV 119
Db 137 TVSS 141
QY 120 TVSS 124

RESULT 5
ID US-08-468-671-2 STANDARD: PPT: 141 AA
XX xxxxxx
XX 01-JAN-1900
XX Sequence 2, Application US/08468671
XX Sequence 2, Application US/08468671
XX Patent No. 5648077
XX GENERAL INFORMATION:
XX APPLICANT: Ostberg, Lars G.
XX TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
XX TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIG
EN
CC NUMBER OF SEQUENCES: 16
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew LLP
CC STREET: Two Embarcadero Center, Eighth Floor
CC CITY: San Francisco
CC STATE: CA
CC COUNTRY: USA
CC ZIP: 94111-3834
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: 08/000,000
CC FILING DATE: 27-MAR-1991
CC PRIOR APPLICATION DATA:

US-08-844-215-5.ral

Thu Feb 26 07:06:06 1998

NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East - Suite 500
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90067

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/10555
FILING DATE: 29-OCT-1993
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:
NAME: Howells, Stacy L.
REGISTRATION NUMBER: 34,842
REFERENCE/DOCKET NUMBER: FD-2630
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 125 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
CLONE: 18/2
FEATURE:

NAME/KEY: Peptide
LOCATION: 1..125
SEQUENCE 125 AA: 13464 MW: 94507 CN:

Query Match 73.7% Score 682; DB 11; Length 125;
Best Local Similarity 73.8% Pred. No. 1,16e-44;
Matches 97; Conservative 18; Mismatches 12; Indels 3; Gaps 4;

Db 1 EVOLVESGGVQVGPGRSLPLSCAASGFTFSYAMSVVRQAPGKGLWVSAISGSGSTTY 60
QY 1 EVOLVESGGVQVGPGRSLPLSCAASGFTFSYAMSVVRQAPGKGLWVSAISGSGSTTY 60
Db 61 ADSVKGRTISRDNKNTLYLQMSLRADTAVYCTGQVLYYG-SCSYHWFDPKGGT 119
QY 61 SDSVKGRTISRDNKNTLYLQMSLRADTAVYCTGQVLYYG-SCSYHWFDPKGGT 118

Db 120 LVTSS 125
QY 119 LVTSS 124

RESULT 7
ID PCT-US93-08435-43 STANDARD; PRT: 122 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 43, Application PC/TUS9308435.

Sequence 43, Application PC/TUS9308435
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham, Corporation
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Navy
APPLICANT: U. S. Government, Secretary of
APPLICANT: the Army
TITLE OF INVENTION: Novel Antibodies for Conferring Passive
TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man

APPLICATION NUMBER: US/08/468,671
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/259,372
FILING DATE: 14-JUN-1994
APPLICATION NUMBER: US 07/871,426
FILING DATE: 21-APR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,036
FILING DATE: 27-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,796
FILING DATE: 15-JUN-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/192,754
FILING DATE: 11-MAY-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/925,196
FILING DATE: 31-OCT-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/904,517
FILING DATE: 05-SEP-1986

ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-50-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 141 AA: 15613 MW: 114738 CN:

Query Match 73.8% Score 683; DB 7; Length 141;
Best Local Similarity 77.0% Pred. No. 9.67e-45;
Matches 97; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

Db 20 QVQLVESGGVQVGPGRSLPLSCAASGFTFSYAMSVVRQAPGKGLWVAVISYDGSNKWY 79
QY 1 EVOLVESGGVQVGPGRSLPLSCAASGFTFSYAMSVVRQAPGKGLWVAVISYDGSNKWY 60
Db 80 ADSVKGRTISRDNKNTLYLQMSLRADTAVYCTGQVLYYG-SCSYHWFDPKGGT 136
QY 61 SDSVKGRTISRDNKNTLYLQMSLRADTAVYCTGQVLYYG-SCSYHWFDPKGGT 119

Db 137 VTYSS 141
QY 120 VTYSS 124

RESULT 6
ID PCT-US93-10555-1 STANDARD; PRT: 125 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 1, Application PC/TUS9310555.

Sequence 1, Application PC/TUS9310555
GENERAL INFORMATION:
APPLICANT: SILVERMAN, GREGG J.
TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
THROUGH
TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
ATES
TITLE OF INVENTION: THEREOF

CC COUNTRY: USA
 CC ZIP: 19477
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: IBM PC compatible
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/08435
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/941,654
 CC FILING DATE: 09-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Bak, Mary E.
 CC REGISTRATION NUMBER: 31,215
 CC REFERENCE/DOCKET NUMBER: SBC P50107
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (215) 540-9200
 CC TELEFAX: (215) 540-5818
 CC INFORMATION FOR SEQ ID NO: 12:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 122 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 122 AA, 13370 MW, 87746 CN;

Query Match 72.4%; Score 670; DB 11, Length 122;
 Best Local Similarity 74.2%; Pred. No. 1,05e-43;
 Matches 92; Conservative 14; Mismatches 16, Indels 2; Gaps 2;

Db 1 EVOLLESGGLVOPGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSEISDGGSYTY 60
 QY 1 EVOLLESGGLVOPGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSEISDGGSYTY 60
 Db 61 PDVTGRTISRDNSKNTLYLQMSLRADTAVYYCAKLIYYG-YDG-YMDYWGQGTIV 118
 QY 61 SDSVKGRFTVSRDNSRNTFLQMSLRPDTAVYYCATFVIFGSIKGRYYLENWGQGTIV 120
 Db 119 TVSS 122
 QY 121 TVSS 124

RESULT 10
 ID US-07-942-245-33 STANDARD; PRT: 125 AA.
 AC xxxxxx
 XX 01-JAN-1900
 DE Sequence 33, Application US/07942245.
 XX Sequence 33, Application US/07942245.
 CC Patent No. 5639641
 CC GENERAL INFORMATION:
 CC APPLICANT: PEDERSEN, Jan T.
 CC APPLICANT: SEARLE, Stephen M.J.
 CC APPLICANT: REES, Anthony R.
 CC APPLICANT: ROGUSKA, Michael A.
 CC APPLICANT: GUILD, Braydon C.
 CC TITLE OF INVENTION: SURFACE PEPTIDIC VENERFING OF POTENT
 CC NUMBER OF SEQUENCES: 52
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Suchrue, Mion, Zinn, Macpeak & Seas
 CC STREET: 2100 Pennsylvania Avenue, N W
 CC CITY: Washington
 CC STATE: D.C.
 CC COUNTRY: United States
 CC FILING DATE: 13-SEP-1994
 CC ZIP: 20037-3202

CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: HP 9000/700 Workstation
 CC SOFTWARE: In house
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/942,245
 CC FILING DATE: 09-SEP-1992
 CC CLASSIFICATION: 530
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (202) 293-7060
 CC TELEFAX: (202) 293-7860
 CC TELETYPE: 6491103
 CC INFORMATION FOR SEQ ID NO: 33:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 125 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 125 AA, 13631 MW, 85784 CN;

Query Match 71.3%; Score 660; DB 7; Length 125;
 Best Local Similarity 69.6%; Pred. No. 6.59e-43;
 Matches 87; Conservative 19; Mismatches 17, Indels 2; Gaps 2;

Db 1 EVOLVOSGGVWOPGRSLRLSCSSGFIFFSYAMVVRQAPGKGLWVA1IWDGSDQHY 60
 QY 1 EVOLVOSGGVWOPGRSLRLSCSSGFIFFSYAMVVRQAPGKGLWVA1IWDGSDQHY 60
 Db 61 ADSVKGRFTISPDNSKNTLYLQMSLRPDTAVYYCATFVIFGSIKGRYYLENWGQGT 120
 QY 61 SDSVKGRFTVSRDNSRNTFLQMSLRPDTAVYYCATFVIFGSIKGRYYLENWGQGT 118
 Db 121 PVTYS 125
 QY 119 LVTYS 123

RESULT 11
 ID US-08-305-683A-2 STANDARD; PRT: 142 AA.
 AC xxxxxx
 XX 01-JAN-1900
 DE Sequence 2, Application US/08305683A.
 XX Sequence 2, Application US/08305683A.
 CC Patent No. 5646041
 CC GENERAL INFORMATION:
 CC APPLICANT: HARFELDT, Elisabeth
 CC APPLICANT: LAKE, Philip
 CC APPLICANT: NOTTAGE, Barbara
 CC APPLICANT: OSTREPG, Lars G.
 CC TITLE OF INVENTION: MONOCLONAL ANTIBODY TO HERPES SIMPLEX
 CC NUMBER OF SEQUENCES: 4
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: IBM PC compatible
 CC SOFTWARE: Patent in Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/305,683A
 CC FILING DATE: 13-SEP-1994
 CC CLASSIFICATION: 424

PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/759,273
CC FILING DATE: 13-SEP-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME:
CC REGISTRATION NUMBER:
CC REFERENCE/DOCKET NUMBER: 37,505
CC REGISTRATION NUMBER: 11823-005230
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2400
CC INFORMATION FOR SEQ ID NO: 2:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 142 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 142 AA: 15758 MW, 111669 CM,
Query Match 71.3%; Score 660; DB 7; Length 142;
Best Local Similarity 71.3%; Pred. No. 6,59e-43;
Matches 89; Conservative 17; Mismatches 13; Indels 5; Gaps 4;
Db 20 QVQLVESGGGVQPGSRSLPLCAASGFTFSVHMWVQAPGKGLQWLAVTWYDGSNKAY 79
QY 1 EVQLLESGGGVQPGSRSLPLCAASGFTFSVHMWVQAPGKGLQWLAVTWYDGSNKAY 60
Db 80 GSVVKGPFITSPDNKNILYLOMNSLRAEDTAVYYCAPGG-VG--PCHFYGLDWMWQPT 136
QY 61 SDVVGKPFITSPDNKNILYLOMNSLRAEDTAVYYCAPGG-VG--PCHFYGLDWMWQPT 118
Db 137 TVTV 140
QY 119 LVTV 122
RESULT 12
ID PCT-US93-07832-21 STANDARD: PRT: 122 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 21, Application PC/TUS9307832
XX
CC Sequence 21, Application PC/TUS9307832
CC GENERAL INFORMATION:
CC APPLICANT: Genentech, Inc.
CC TITLE OF INVENTION: Immunoglobulin variants
CC NUMBER OF SEQUENCES: 40
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Genentech, Inc.
CC STREET: 460 Point San Bruno Blvd
CC CITY: South San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94080
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: 5 25 inch, 360 kb floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patin (Genentech)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/07832
CC FILING DATE: 19930820
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/715272
CC FILING DATE: 14-JUN-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/05126
CC FILING DATE: 15-JUN-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/934373

PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/759,273
CC FILING DATE: 13-SEP-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME:
CC REGISTRATION NUMBER:
CC REFERENCE/DOCKET NUMBER: 37,505
CC REGISTRATION NUMBER: 11823-005230
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2400
CC INFORMATION FOR SEQ ID NO: 21:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC SEQUENCE 122 AA: 13077 MW: 86439 CN,
Query Match 71.3%; Score 658; DB 11; Length 122;
Best Local Similarity 75.2%; Pred. No. 9,51e-43;
Matches 94; Conservative 15; Mismatches 12; Indels 4; Gaps 4;
Db 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFSVAMSVWVQAPGKGLWVSVISGGGSTYY 60
QY 1 EVQLVESGGGLVQPGGSLKLSCAASGFTFSVAMSVWVQAPGKGLWVSVISGGGSTYY 60
Db 61 ADSVKGPFITSPDNKNILYLOMNSLRAEDTAVYYCAPGGVGY-SLSG-LY-DYWGQGTLL 117
QY 61 SDVVGKPFITSPDNKNILYLOMNSLRAEDTAVYYCAPGGVGY-SLSG-LY-DYWGQGTLL 119
Db 118 TVVSS 122
QY 120 TVVSS 124
RESULT 13
ID US-08-478-030-04 STANDARD: PRT: 123 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 94, Application US/08478039.
XX
CC Sequence 94, Application US/08478039
CC Patent No. 5681722
CC GENERAL INFORMATION:
CC APPLICANT: Newman, Roland A.
CC APPLICANT: Hanna, Nabil
CC APPLICANT: Raab, Ronald W.
CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CC NUMBER OF SEQUENCES: 114
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
CC STREET: 699 Prince St.
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/478,039
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 09,279,072
CC FILING DATE: 25-JAN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/912,292
CC FILING DATE: 10-JUL-1992
CC PRIOR APPLICATION DATA:

CC	APPLICATION NUMBER:	US-98/211,202
CC	FILING DATE:	23-SEP-1992
CC	CLASSIFICATION:	435
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	GB 9120252.3
CC	FILING DATE:	23-SEP-1991
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	GB 9120377.8
CC	FILING DATE:	25-SEP-1991
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	GB 9206318.9
CC	FILING DATE:	24-MAR-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	GB 9206372.6
CC	FILING DATE:	24-MAR-1992
CC	PRIOR APPLICATION DATA:	
CC	APPLICATION NUMBER:	PCT/GB92/00883
CC	FILING DATE:	15-MAY-1992
CC	ATTORNEY/AGENT INFORMATION:	
CC	NAME:	David W. Clough
CC	REGISTRATION NUMBER:	46,107
CC	REFERENCE/DOCKET NUMBER:	28111/31940
CC	TELECOMMUNICATION INFORMATION:	
CC	TELEPHONE:	312-474-6300
CC	TELEFAX:	312-474-0448
CC	TELEX:	25-3856
CC	INFORMATION FOR SEQ ID NO:	141:
CC	SEQUENCE CHARACTERISTICS:	
CC	LENGTH:	116 amino acids
CC	TYPE:	amino acid
CC	TOPOLOGY:	linear
CC	MOLECULE TYPE:	protein
CC	SEQUENCE	115 AA; 12678 MW; 72426 CN;
CC	Query Match	70.7%; Score 655; DA 6; Length 116;
CC	Best Local Similarity	76.1%; Pred No 1 65e-42;
CC	Matches	89; Conservative 15; Mismatches 12; Indels 1; Gaps 1;
Db	1	OVQLVESGGVVQVQPSLPLSCAASGTFESSAMHWVRGAPGKGLFWAVISYDGSNKYY 60
QY	1	EVQLLESQGVVQVQPSLPLSCAASGTFESSAMHWVRGAPGKGLFWAVISYDGSNKYY 60
Db	61	ADSVAGRTISPDNSKNTLYLQMSLPEDTAVVYVCASGP-VCSGSGCSPPDYWQG 116
QY	61	SUSVAGRTISPDNSKNTLYLQMSLPEDTAVVYVCATEVLFISIKGRYYLENWQG 117
RESULT	15	
ID	PCT-US93-10555-6	STANDARD: PRT: 125 AA.
XX	XXXXXX	
DT	01-JAN-1900	
DE	Sequence 6, Application PC/TUS9310555.	
XX	Sequence 6, Application PC/TUS9310555	
CC	GENERAL INFORMATION:	
CC	APPLICANT:	SILVERMAN, GREGG J.
CC	TITLE OF INVENTION:	METHOD FOR STIMULATING PRODUCTION OF
CC	TITLE OF INVENTION:	VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
CC	THROUGH	
CC	TITLE OF INVENTION:	VACCINATION WITH A R-CELL SUPERANTIGEN AND CONJUG
ATES		
CC	TITLE OF INVENTION:	THEREOF
CC	NUMBER OF SEQUENCES:	51
CC	CORRESPONDENCE ADDRESS:	
CC	ADDRESSEE:	Spensley Horn Jubas & Lubitz
CC	STREET:	1880 Century Park East - Suite 500
CC	CITY:	Los Angeles
CC	STATE:	California
CC	COUNTRY:	USA
CC	ZIP:	90067

CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/COCKET NUMBER: FD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 6:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 125 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC IMMEDIATE SOURCE:
CC CLONE: RIV
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1..125
CC SEQUENCE 125 AA: 13512 MW: 90692 CN:

Query Match 70.6%; Score 654; DB 11; Length 125;
Best Local Similarity 72.0%; Pred. No. 1.98e-42;
Matches 90; Conservative 15; Mismatches 19; Indels 1; Gaps 1;

Db 1 EVOLVESGGGVVQPGSSSLPLSCAASGFTFSFAMHWVQAPGKGLEWVAVMSYSGENKYY 60
QY 1 EVOLLESGGGVVQPGRSPLSLSCAASGFTFSAYGMHWVQAPGKGLEWVAGIWFDSNQYY 60

Db 61 VDSVKGRFTISPSNKNLTLYLQMNLSLPAEDTALYYCAKLSTAASGFIFETYGMEWQGITL 120
QY 61 SDSVKGRFTVSPNSNTLFLQMNLSLPPEDTAVYYCAT-EVLFSGSIKGPYYLENWGQGITL 119

Db 121 VTVSS 125
QY 120 VTVSS 124

Search completed: Tue Feb 24 07:39:21 1998
Job time : 5 secs.



WQ5REH
***** (TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:12:31 1998; Maspar time 7.36 Seconds
234.122 Million cell updates/sec

Tabular output not generated

Title: >US-08-844-215-5
Description: (1-124) from USC8844.15.pep
Perfect Score: 926
Sequence: 1 EVQLLEGGGQVGPGRSLRL IKGPYLENKGQITLVSS 124

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq30
1 part:1 2 part:2 3 part:3 4 part:4 5 part:5 6 part:6 7 part:7
8 part:8 9 part:9 10 part:10 11 part:11 12 part:12 13 part:13
14 part:14 15 part:15 16 part:16 17 part:17 18 part:18
19 part:19 20 part:20 21 part:21 22 part:22 23 part:23

Statistics: Mean 30.371; Variance 159.298; scale 0.191

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description	Pred. No.
1	705	76.2	192	7	R38161	Sequence of the heavy	5.59e-46
2	695	75.1	119	18	R95216	Human foetal immunogl	5.74e-45
3	692	74.7	123	23	W15534	Anti-TGF beta-1 scfv	9.96e-45
4	691	74.6	123	23	W15531	Anti-melanoma antibody	1.20e-44
5	690	74.5	111	2	R12275	Anti-human Rhd HAM-R	1.44e-44
6	685	74.0	115	4	R22571	Heavy chain VH3.5 fro	3.60e-44
7	684	73.9	120	17	R52064	Heavy chain variable	4.33e-44
8	683	73.8	123	23	W15535	Anti-TGF beta-1 scfv	5.20e-44
9	683	73.8	141	19	W01522	Monoclonal antibody P	5.20e-44
10	683	73.8	141	23	W24984	Monoclonal antibody P	5.20e-44
11	681	73.5	506	2	R12134	GpF 3 of 4B9 human MA	7.51e-44
12	677	73.1	143	9	R54047	Sequence of the VH re	1.57e-43
13	674	72.8	122	9	R50315	Humanised heavy chain	2.72e-43
14	673	72.7	125	9	P54784	SPA-reactive IgM heav	3.26e-43
15	672	72.6	122	9	R50312	Humanised heavy chain	3.92e-43
16	671	72.5	115	23	W15522	Anti-TGF beta-2 scfv	4.71e-43
17	670	72.4	122	9	R50311	Humanised heavy chain	5.66e-43
18	669	72.2	126	5	R28746	Heavy chain variable	6.80e-43
19	668	72.1	140	23	W15524	Anti-melanoma antibody	8.17e-43
20	664	71.7	117	12	R66323	Human immunoglobulin	1.70e-42

21	664	71.7	123	23	W15536	Anti-TGF beta-1 scfv	1.70e-42
22	664	71.7	126	7	P06512	KOI heavy chain	1.70e-42
23	662	71.5	112	2	R12274	Anti-human Rhd REG-A	2.46e-42
24	662	71.5	141	13	P75393	Anti-interleukin-1-31	2.46e-42
25	660	71.2	142	23	W22551	64-963 antibody HSV86	3.55e-42
26	660	71.3	221	10	P56234	162-109/110-61/H-125	3.55e-42
27	656	70.9	459	8	R42066	Human anti-RS heavy	7.39e-42
28	654	70.6	135	9	P54789	SPA-reactive IgM heav	1.07e-41
29	654	70.6	135	9	P54789	SPA-reactive IgM heav	1.07e-41
30	653	70.5	124	23	W15537	Anti-melanoma antibody	1.28e-41
31	652	70.4	117	12	R66321	Human immunoglobulin	1.54e-41
32	652	70.4	119	20	W19225	Heavy chain #3 for an	1.54e-41
33	648	70.0	123	23	W09592	Human antibody C4.1 h	3.20e-41
34	648	70.0	140	14	P80480	Anti-human IL-4 human	3.20e-41
35	648	70.0	487	14	P80617	Anti-human IL-4 human	3.20e-41
36	644	69.5	117	23	W15523	Anti-TGF beta-2 scfv	6.67e-41
37	642	69.3	142	5	P31534	MH4H7 MA5 heavy chain	9.62e-41
38	641	69.2	132	6	P30773	Consensus humanised m	1.16e-40
39	641	69.2	140	19	W06205	Xenograft antibody HA	1.16e-40
40	640	69.1	116	6	P24225	Human TNF binding ant	1.39e-40
41	640	69.1	117	17	R52065	Heavy chain variable	1.39e-40
42	640	69.1	118	20	W13921	Heavy chain #1 for an	1.39e-40
43	639	69.0	123	12	R69084	Anti-HIV Fab rev9(VH3	1.67e-40
44	639	69.0	123	22	W08733	Human anti-HIV Fab am	1.67e-40
45	639	69.0	134	23	W15533	Anti-melanoma antibody	1.67e-40

ALIGNMENTS

RESULT 1
ID R38161 standard; Protein: 192 AA.

AC P38161;
DI 01-OCT-1993 (first entry)
DE Sequence of the heavy chain variable region (VH) of human
DE immunoglobulin G3 (IgG3) produced by transformed human B-cell line
DE 88BV59, ATCC CRL 10624.
KW B-cell; immunoglobulin g; cancer; tumour.

GS Homo sapiens.

EH Key Location/Qualifiers

FT Region 1..113

FT /label= VAR

FT /note= "1st AA is denoted AA#1"

FT Region 31..49

FT /label= CDR 1

FT Region 50..94

FT /label= CDR 2

FT Region 95..111

FT /label= CDR 3

FT Region 112..223

FT /label= CH 1

FT Region 224..238

FT /label= Hinge

FT Region 239..242

FT /label= Fab'

PN EP-546634-A.

PD 16-JUN-1993.

PE 29-DEC-1992. 203827.

PP 14-DEC-1991. US-807300.

PA (ALKU) AK20 NV.

PI Crichton V2. Haspel MV, Kobrin BJ,

DR WP1.93-193019/24.

DE N-F52B. Q43772.

DE Transformed human B-cell line for monoclonal antibody produ. for

PT cancer diagnosis - prepd from peripheral blood B-cells of cancer

PT patients actively immunised with autologous tumour antigen, for

PT treating cancers

PS Claim 5; Fig 2, 18pp; English.

CC Q43772 encodes the complete heavy chain from the leader through AAs

CC 212. 88BV59 uses VH11 and a D region which may have resulted from

CC intra D-D recombination and/or gene conversion along with somatic

CC mutation. It is radically different from any germ line D region. It

CC utilises germ line JH3. It is of note that a cysteine at AA posn. 59

CC (AA No. 78 in R38161) is present within the 88BV59 VH. No other

CC human variable region heavy chains have a cysteine at this posn. i.e.
 CC Kabat posn. 59.
 SQ Sequence 192 AA:

Query Match 76.2%; Score 706; DB 7; Length 192;
 Best Local Similarity 77.0%; Pred. No. 7.59e-46;
 Matches 97; Conservative 14; Mismatches 12; Indels 3; Gaps 3;
 Db 20 qvqlvesggvqgrrslrlscaasgftfssygmhwrrqapkgldwvavisdgskyy 79
 QY 1 EVQLLESGGGVQVQGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLWVAGIWFVDSNQYY 60
 Db 80 adsvkgrftisrdnsnkntlylqmslraedtavvycvkeg-fgsvvvtthlafdwggqt 138
 QY 61 SDSVKGRFTVSRNRTFLQWNSLRPEPTAVYICATEVLFSGIKGRYYLENNWVQGTIV 118

Db 139 mvtvss 144
 QY 119 LVTSS 124

RESULT 2
 ID R95216 standard; protein; 119 AA.
 AC R95216; 1996 (first entry)
 DT 16-DEC-1996
 DE Human foetal immunoglobulin 5opl'CL variable heavy chain.
 KW Antibody; fusion protein; single chain; inhibition; tumour;
 KW diagnosis; detection; imaging; immunotoxin; targeting; assay;
 KW immunoassay; Lewis(Y) carbohydrate antigen.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 31..35
 FT /label= CDR 1.
 FT Domain 50..66
 FT /label= CDR 2.
 FT Domain 99..108
 FT /label= CDR 3.
 FT WO9613594-A1.
 PN 09-MAY-1996.
 PD 26-OCT-1995; U13811.
 PF 28-OCT-1994; US-331398.
 PR 28-OCT-1994; US-331396.
 PR 28-OCT-1994; US-331397.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee B;
 PI Padlan EA, Pai L, Pastan I, Willingham M;
 DR WPI: 96-251462/25.
 PT Single chain fusion proteins and antibodies - useful to diagnose and
 PT treat cancer, specifically bind Lewis(Y) related carbohydrate
 PT antigen

PS Example 13; Figure 11A; 116pp; English.
 CC A novel recombinant DNA molecule which encodes a single chain fusion
 CC protein or antibody comprising the Fv region of both the light and
 CC heavy chains of an antibody (Ab) fused together, and an effector
 CC molecule, where the fusion protein or Ab has the binding specificity
 CC of monoclonal Ab (MAB) B1, B3 or B5, can be used for the production
 CC of such fusion proteins or antibodies. The fusion proteins can be
 CC used in compositions as an immunotoxin to inhibit tumour cell growth.
 CC The single chain antibody can be used to detect the presence or
 CC absence of cells bearing a Lewis(Y) carbohydrate antigen in a
 CC patient. The antibodies are also useful as multiple targeting
 CC moieties, providing at least 2 kinds of biological activity. They
 CC can also be used in diagnostic assays and for the imaging of tumours
 CC when attached to a radiolabel and for the pathological diagnosis of
 CC tumours. Humanised antibodies are less immunogenic than the mouse
 CC Mabs B1, B3 and B5, making them more suitable for long term
 CC treatment.
 SQ Sequence 119 AA;

Query Match 75.1%; Score 695; DB 18; Length 119;
 Best Local Similarity 78.2%; Pred. No. 5.74e-45;
 Matches 97; Conservative 14; Mismatches 8; Indels 5; Gaps 2;
 Db 1 qvqlvesggvqgrrslrlscaasgftfssygmhwrrqapkgldwvavisdgskyy 60
 QY 1 EVQLLESGGGVQVQGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLWVAGIWFVDSNQYY 60
 Db 61 adsvkgrftisrdnsnkntlylqmslraedtavvycvkeg-fgsvvvtthlafdwggqt 119

Db 1 qvqlvesggvqgrrslrlscaasgftfssygmhwrrqapkgldwvavisdgskyy 60
 QY 1 EVQLLESGGGVQVQGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLWVAGIWFVDSNQYY 60
 Db 61 adsvkgrftisrdnsnkntlylqmslraedtavvycvkeg-fgsvvvtthlafdwggqt 115
 QY 61 SDSVKGRFTVSRNRTFLQWNSLRPEPTAVYICATEVLFSGIKGRYYLENNWVQGTIV 120
 Db 116 tvss 119
 QY 121 TVSS 124

RESULT 3
 ID W15534 standard; protein; 123 AA.
 AC W15534;
 DT 27-NOV-1997 (first entry)
 DE Anti-TGF beta-1 scFv antibody 1-B2 VH domain.
 KW Transforming growth factor beta-1; TGF-beta-1; human;
 KW antibody engineering; scFv; phage display; lung fibrosis;
 KW arterial injury; proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis;
 KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection; therapy.
 OS Homo sapiens.
 FH GB2305921-A.
 FN 23-APR-1997.
 PD 07-OCT-1996; 020920.
 PR 19-JAN-1996; GB-001081.
 PR 06-OCT-1995; GB-020486.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
 PI Wilton AJ;
 DR WPI: 97-215350/20.
 DR N-PSDB; T60380.

PT Agent contg. antigen-binding domain of human antibody to
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
 PT immune and inflammatory disease.
 PS Claim 16; Fig 1a(1); 184pp; English.
 CC This polypeptide sequence comprises the VH domain of human scFv
 CC antibody 1B2 (also known as 7A3), which is specific for
 CC transforming growth factor (TGF) beta-1. It is encoded by a gene
 CC (T60380) isolated from a peripheral blood lymphocyte library. The
 CC antigen-binding domains of human antibodies (see W15522-40) to TGF
 CC beta-1 and/or beta-2 can be used to counter the adverse effects of
 CC TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or
 CC keloid scarring, lung fibrosis, arterial injury, proliferative
 CC retinopathy, retinal detachment, adult respiratory distress syndrome,
 CC liver cirrhosis, post myocardial infarction, post-angioplasty
 CC restenosis, scleroderma, vascular disorders, cataract, glaucoma, or
 CC esp. neural scarring and glomerulonephritis, also (not claimed)
 CC osteoporosis), or (ii) immune and inflammatory diseases (rheumatoid
 CC arthritis, macrophage deficiency diseases or macrophage pathogen
 CC infection). Nucleic acids encoding human antibody VH and VL can be
 CC used for produ. of recombinant antigen-binding domains. These are
 CC highly specific, have low dissociation constants (pred. less than 5
 CC nM) and low IC50s for neutralisation.
 SQ Sequence 123 AA;

Query Match 74.7%; Score 692; DB 23; Length 123;
 Best Local Similarity 75.8%; Pred. No. 9.96e-45;
 Matches 94; Conservative 15; Mismatches 14; Indels 1; Gaps 1;

Db 1 qvqlvesggvqgrrslrlscaasgftfssygmhwrrqapkgldwvavisdgskyy 60
 QY 1 EVQLLESGGGVQVQGRSLRLSCAASGFTFSAYGMHWVRQAPGKGLWVAGIWFVDSNQYY 60
 Db 61 adsvkgrftisrdnsnkntlylqmslraedtavvycvkeg-fgsvvvtthlafdwggqt 119

QY 61 SDSVKGPFVTSNSENFLFUMNSLPEDTAVVYCAIEVLFQSGKSGYVLENWQGTLLV 120
 Db 120 vtss 123
 QY 121 TVSS 124

RESULT 4
 ID WL331 standard; protein: 123 AA.
 AC WL331:
 DT 28-OCT-1997 (first entry)
 DE Anti-melanoma antibody heavy chain clone V575.
 KW Human; monoclonal antitumor antibody; peripheral blood lymphocyte.
 KW cancer; tumorigenesis; anticancer vaccine.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 31..35
 FT /label= CDR1
 FT Region 50..66
 FT /label= CDR2
 FT Region 100..113
 FT /label= CDR3
 PN WC9702479-A2
 PD 23-JAN-1997.
 PF 28-JUN-1996; IB1032.
 PR 30-JUN-1995; US-497647.
 PA (UYVA) UNIV YALE.
 PI Cai X, Garen A;
 DR WPI: 97-109061/10.
 PT Prodn. of human monoclonal anti-tumour antibodies - by screening a fusion phase library produced using peripheral blood lymphocytes from a cancer patient
 PS Claim 19: Page 68; 82pp; English.
 CC A process for isolating and synthesising human monoclonal anti-tumour antibodies has been produced. The process involves: (a) constructing at least one fusion phase library from the peripheral blood lymphocytes (PBLs) of a cancer patient; (b) screening for anti-tumour antibodies in the phase library in a binding assay with cultured tumour cells of the same type as the patient's tumour; (c) removing extraneous antibodies by absorption against normal human cells; (d) cloning the phase selected in step (b) and (c); (e) assaying the specificity of the cloned phase by incubating the phase with at least two types of cultured normal cells; and (f) further testing the specificity of cloned phase that do not bind to either cell line of cultured normal cells in further binding assays to cultured tumour cells derived from more than one other tumour that is not the patient's tumour. The present sequence represents a human heavy chain antibody, from an scFv antibody fusion phase library, produced by a method as described above. The antibodies produced can be used for diagnostic and therapeutic applications and for isolating tumour antigens for studying tumourigenesis or for use as anti-cancer vaccines. The human antibodies have low immunogenicity in humans compared to murine monoclonal antibodies (MABs). Since the antibodies are isolated from fusion phase libraries, their affinity and specificity for a tumour cell line can be improved by genetic manipulations.
 SQ Sequence 123 AA;

Query Match 74.6%; Score 631; DB 23; Length 123.
 Best Local Similarity 75.0%; Pred. No 1.20e-44;
 Matches 93; Conservative 17; Mismatches 12; Indels 2; Gaps 2;
 Db 1 qqlvsgggvqprslrlscasagftfssygmhwvrgqpkglwvavlysgnkyr 60
 QY 1 EVOLLESGGGVQPRSLRLSCAASGFTFSAYGMHWVFPQAPGKLEWVAGIWFDPGSGNOY 60
 Db 61 adsvkgrftisrdnsrnlflqmnsrlrpedtavyvycargfygg-nsdygmddwbqtq 119
 QY 61 SDSVKGPFVTSNSENFLFUMNSLPEDTAVVYCAIEVLFQSGKSGYVLENWQGTLL 119
 Db 120 vtvs 123
 QY 120 VTVS 123

RESULT 5
 ID R12275 standard; Protein: 111 AA.
 AC R12275:
 DT 15-AUG-1991 (first entry)
 DE Anti-human Phd HAM-R MAB (VH chain)
 KW Monoclonal antibody; rhesus D; blood-typing; CDR;
 KW haemolytic disease of the newborn; HDN.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 23..27
 FT /label= CDR1
 FT Region 42..58
 FT /label= CDR2
 FT Region 91 106
 FT /label= CDR3
 PN W09107492-A.
 PD 30-MAY-1991.
 PF 13-NOV-1990; E01964.
 PP 13-NOV-1989; GR-025590
 PA (BLOO-) CENT BLOOD LAB AUTH.
 PI Hughes- Jones N;
 DR WPI: 91-178104/24.
 DR N-PSDB: Q11957
 PT DNA encoding complementary determining regions - of human anti-rhesus D antibodies, useful in prodn. of monoclonal antibodies and for passive immunisation
 PS Disclosure, Fig 14, 32pp, English.
 CC The DNA sequence of eleven monoclonal antibodies are represented in Q119145-57. Synthetic genes, for both heavy and light chains may be created by combining selected CDR 1, 2, and 3 regions, which may be selected from different antibody mols, having varied binding specificity. The chimaeric anti-Rhd antibodies can be used for diagnosis and therapy and are capable of providing blood-typing reagents of high specificity and reliability. They can also be used in passive immunisation to prevent haemolytic disease of the newborn
 CC Sequence 111 AA;

Query Match 74.5%; Score 590; DB 2; Length 111.
 Best Local Similarity 79.8%; Pred. No 1.44e-44;
 Matches 89; Conservative 13; Mismatches 7; Indels 3; Gaps 3;
 Db 1 ggvvqprslrlscasagftfssygmhwvrgqpkglwvavlysgnkyrvadskgrf 60
 QY 9 GGVVQPRSLRLSCAASGFTFSAYGMHWVFPQAPGKLEWVAGIWFDPGSGNOYSDSVKGRPF 68
 Db 61 tirdskntlylqmslrtaedtavvycargfygg-ryygmddwbqpgt 111
 QY 69 TVSEKNSNLEFLQMSLRLPEDEFAVYCAIEV-LFQSGKSGYVLENWQGTLL 118

RESULT 6
 ID R22571 standard; Protein: 115 AA.
 AC R22571:
 DT 21-MAY-1992 (first entry)
 DE Heavy chain VH3.5 from BSA binding scFv fragment.
 KW FU, bacteriophage, gene III, filamentous, phagemid, capsid, coat,
 KW Pilius, g3p, binding, adsorption; gene VII; diverse repertoire,
 KW specific binding pairs, replicable genetic display package, human.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 10-JUL-1990; GR-015198.
 PF 10-JUL-1990; GR-015198.
 PP 19-OCT-1990; GR-023845.
 PP 12-NOV-1990; GR-024593.
 PR 06-MAR-1991; GB-004744.
 PR 15-MAY-1991; GB-010549.
 PA (CAMP-) CAMPRIPE ANTIBODY.
 PA (MEDI-) MED RES COUNCIL.
 PI McCafferty J, Pape AP, Johnson KS, Hoogenboom HPJ, Griffiths AD; Jackson PH, Holliger KP, Marks JD, Jackson TP, Chiswell DJ;

therapeutic efficiency by presenting human surface on V-region
 Example 1; Fig 4B; 230pp; English.
 PS Modification of a rodent antibody (Ab) or fragment by resurfacing in
 CC order to produce a humanised rodent Ab can be determined by calculating
 CC homology between murine and human Ab antibody surfaces. In order to test
 CC the resurfacing approach of the invention, three humanisation experiments
 CC were set up: (1) traditional loop grafting; (2) resurfacing approach
 CC using most similar chain; and (3) resurfacing approach using human
 CC sequences with similar surface residues. The Ab used was the murine
 CC anti-N901 Ab (see R52064). Experiment 2 was carried out using the present
 CC sequence which represents the human G36005 Ab heavy chain variable region
 CC with 89 percent homology with anti-N901 Ab. N901/G36005 (R52065) was
 CC prep'd by CPE grafting. Sequence numbering starts at 118 in the
 CC specification.
 CC Sequence 120 AA:
 SQ
 Query Match 73.9%; Score 684; DB 17; Length 120;
 Best Local Similarity 77.2%; Pred. No. 4.31e-44;
 Matches 95; Conservative 14; Mismatches 11; Indels 3; Gaps 2;
 Db 1 qvqlvesggvqpqrslriscasgftfssygmhvwrgapkglewavysydgskyy 60
 Qy 1 EVQLLESGGVGWVQFGRSRLSCAASGFTFSAYGMHWVPQAPKCLEFWVAIMFDGSNOYY 60
 Db 61 adsvkgrftisrdnsntlylqmnsrlrpedtavyycatevlfgsikgrylennwqogt 117
 Qy 61 SDSVKGRFTVSRNSRNTLFLQNSLRPEDTAVYYCATEVLFGSIKGRYVLENNWQGTIV 120
 Db 118 tvs 120
 Qy 121 TVS 123
 RESULT 8
 ID W15535 standard; Protein: 123 AA.
 AC W15535.
 DT 21-NOV-1997 (first entry)
 DE Anti-TGF beta-1 scfv antibody 3109 VH domain.
 KW Transforming growth factor beta-1; TGF-beta-1; human;
 KW antibody engineering; scfv; phage display; lung fibrosis;
 KW arterial injury; proliferative retinopathy; retinal detachment;
 KW adult respiratory distress syndrome; liver cirrhosis;
 KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW rheumatoid arthritis; osteoporosis; immune disease; inflammation;
 KW macrophage pathogen infection; deficiency disease;
 OS Homo sapiens.
 PN GB2305921-A.
 PD 23-APR-1997.
 PF 07-OCT-1996; 020920.
 PR 19-JAN-1996; GB-001081.
 PR 06-OCT-1995; GB-020486.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
 PI Wilton AJ;
 DR WPI: 97-215360/20.
 DR N-PSDB: T60381.
 PT Agent contg. antigen-binding domain of human antibody to
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
 PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
 PT Immune and inflammatory disease
 PS Claim 16; Fig 1a(ii); 184pp; English.
 CC This polypeptide comprises the VH domain of human scfv antibody
 CC 3109, which is specific for transforming growth factor (TGF)
 CC beta-1. It is encoded by a gene (T60381) isolated from a large
 CC single chain Fv library. The antigen-binding domain of human
 CC antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can be used
 CC to counter the adverse effects of TGF beta, such as (i) promotion
 CC of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis,
 CC arterial injury, proliferative retinopathy, retinal detachment,
 CC adult respiratory distress syndrome, liver cirrhosis, post

Winter GP, Bonnett TP;
 WPI: 92-056862/07.
 PI Producing members of specific binding pairs - by expression in
 PI recombinant host cells with a secreting replicable genetic
 PT display package.
 PS Table 11; Page 152; 109pp; English.
 CC PCR was used to prepare a human scfv library from RNA from white
 CC blood cells from an unimmunised donor. Heavy chains from IgG and
 CC IgM antibodies were amplified separately. Four separate libraries
 CC were generated (IgG-K, IgG-lambda, IgM-K and IgM-lambda). The
 CC purified scfv fragments were ligated into the phagemid pHEM1 for
 CC expression on the surface of fd bacteriophage as gene III fusions.
 CC The clones were then subjected to affinity selection for binding
 CC to pHOX:BSA by selection on tubes followed by analysis by ELISA. Of
 CC 96 clones analysed, 43 showed binding to both pHOX:BSA and BSA.
 CC These were designated BSA binders. Thirteen of fourteen clones
 CC sequenced had the same sequence, the VH derived from a human VH3
 CC family gene (shown here) and the VL from a human V lambda 3 family
 CC gene (R22572). The other was derived from a human VH4 family gene
 CC and a human VK1 family gene. One clone bound only to pHOX:BSA
 CC (oxazolone binder). This sequence revealed a VH derived from a
 CC human VH1 family gene (P22569) and VL from a human V lambda 1
 CC family gene (R22570).
 CC See also R21260-307, 309-312, P22450, P22565, P22567-81
 CC Sequence 115 AA:
 SQ
 Query Match 74.0%; Score 685; DB 4; Length 115;
 Best Local Similarity 78.0%; Pred. No. 3.60e-44;
 Matches 92; Conservative 14; Mismatches 9; Indels 3; Gaps 3;
 Db 1 qvqlvesggvqpqrslriscasgftfssygmhvwrgapkglewavysydgskyy 60
 Qy 1 EVQLLESGGVGWVQFGRSRLSCAASGFTFSAYGMHWVPQAPKCLEFWVAGIMFDGSNOYY 60
 Db 61 adsvkgrftisrdnsntlylqmnsrlrpedtavyycatevlfgsikgrylennwqogt 115
 Qy 61 SDSVKGRFTVSRNSRNTLFLQNSLRPEDTAVYYCATEVLFGSIKGRYVLENNWQGT 118
 RESULT 7
 ID R52064 standard; Protein: 120 AA.
 AC R52064;
 DT 11-OCT-1996 (first entry)
 DE Heavy chain variable region of human G36005 antibody.
 KW antibody; humanised; murine; human; heavy chain; light; variable;
 KW framework region; complementarity determining region; reshaping;
 KW modelling; surface residue; modify.
 OS Homo sapiens.
 PN Key Location/Qualifiers
 FT Region 1..30
 FT /label= framework_region_1
 FT /note= "FR 1"
 FT Region 31..35
 FT /label= complementarity_determining_region_1
 FT /note= "CDR 1"
 FT Region 36..49
 FT /note= "FR 2"
 FT Region 50..59
 FT /note= "CDR 2"
 FT Region 60..98
 FT /note= "FR 3"
 FT Region 99..110
 FT /note= "CDR 3"
 PN EP-592106-A1.
 PD 13-APR-1994.
 PF 07-SEP-1993; 307051.
 PR 09-SEP-1992; US-942245.
 PA (PEDE/) PEDERSEN J T.
 PA (IMMU-) IMMUNOGEN INC.
 PI Guld BC, Pedersen JT, Rees AP, Roguska MA, Searle SMJ;
 DR WPI: 94-120230/15.
 PT Method of resurfacing of rodent antibodies to produce humanised
 PT antibody forms - for producing non-human antibodies with improved

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CC This is the amino acid sequence of the heavy chain variable (Vh) region
 CC from the human monoclonal antibody (MAB) PE1-1. The MAB was generated
 CC by immunising humans with a hepatitis B virus (HBV) vaccine, isolating
 CC peripheral blood lymphocytes (PBL) and fusing them with a mouse/human
 CC xenogeneic cell line SP2-4. 5 cell lines were isolated: PE1-1, ZM1-1,
 CC ZM1-2, MD3-4 and LO3-3. The cell lines were then tested for production
 CC of an anti-hepatitis B virus surface antigen antibody by ELISA. The MABs
 CC are then purified from large scale cell culture by protein A
 CC chromatography, size separation on Sephacryl S300 gel and ion exchange
 CC chromatography on Q-Sepharose. The heavy and light chains of the MABs
 CC were isolated and their amino acid sequences determined. Primers were
 CC generated and used to amplify cDNA synthesised from RNA purified from
 CC each hybridoma cell line. The sequences of the heavy and light chains
 CC (nucleic acid and amino acid) from MABs PE1-1, ZM1-2 and MD3-4 are
 CC shown in T85838-45 and W24984-91. The MABs can be used to treat HBV
 CC infections in immunosuppressed patients or patients with chronic active
 CC hepatitis, especially liver transplant patients.
 SQ Sequence 141 AA;

Query Match 73.8%; Score 683; DB 23; Length 141;
 Best Local Similarity 77.6%; Pred. No. 5.20e-44;
 Matches 97; Conservative 10; Mismatches 14; Indels 4; Gaps 2;

DB 20 qvqlvesggvqpgsrslrslscasgftfrsrygmhwrqapqgkglewvavissdgsdyj 79
 QY 1 EVQLLESGGCVQPGSRSLRSLSCAASGFTFSAYGMHWRQAPQPGKGLWVAVIGWFGDSNOYY 60
 DB 80 adavkgrftisrdnsrtdmlyvqgnsrardtavyvysakakcsqg scysyfdywdqgtily 136
 QY 61 SDSVKGRFTVSRNSRNTLFLQMSLRPDTAVYVCATEVLFGSIKGRYVLENWQGJTL 119
 DB 137 vtvs 141
 QY 120 VTVSS 124

RESULT 11
 ID R12134 standard; Protein: 506 AA.
 AC R12134;
 DT 01-AUG-1991 (first entry)
 DE ORF 3 of 4B9 human MAB heavy chain variable region clone.
 KW immunoglobulin G; heavy chain; variable region; duplication,
 KW passive immunity; group B streptococci.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 244...369
 FT /label= L'V region
 FT /note= "last 3 residues of leader and variable
 FT region; the rest of leader is translated in
 FT ORF 1"
 PN WO9106305-A.
 PD 16-MAY-1991.
 PF 06-NOV-1990; U06426.
 PR 07-NOV-1989; US-432700.
 PA (BRIM) BRISTOL-MYERS SQUIB.
 PI Shuford WM, Harris LJ, Raffi HV;
 DR WPI: 91-163947/22.
 DR N-PSDB: Q11880.
 PT Oligomeric immunoglobulin(s) with high avidity for antigen(s) -
 PT formed by duplicating esp. variable region of light chain of IgG
 PT class
 PS Example 4; Fig 18; 104pp; English.
 CC This sequence is derived from the nucleotide sequence encoding the
 CC heavy chain variable region. The "x" residues represent nonsense
 CC codons. The coding sequence has been translated in all 3 reading
 CC frames (see also R12132 and R12133).
 CC See also Q11878 and Q11879.
 SQ Sequence 506 AA;

Query Match 73.5%; Score 681; DB 2; Length 506;
 Best Local Similarity 76.6%; Pred. No. 7.51e-44;
 Matches 95; Conservative 14; Mismatches 13; Indels 2; Gaps 1,

DB 247 qvqlvesggvqpgsrslrslscasgftfrsrygmhwrqapqgkglewvavissdgsdyj 406
 QY 1 EVQLLESGGCVQPGSRSLRSLSCAASGFTFSAYGMHWRQAPQPGKGLWVAVIGWFGDSNOYY 60
 DB 307 adavkgrftisrdnsrtdmlyvqgnsrardtavyvysakakcsqg scysyfdywdqgtily 464
 QY 61 SDSVKGRFTVSRNSRNTLFLQMSLRPDTAVYVCATEVLFGSIKGRYVLENWQGJTL 120
 DB 365 tvss 368
 QY 121 VTVSS 124
 RESULT 12
 ID R54047 standard; Protein: 143 AA.
 AC R54047;
 DT 08-NOV-1994 (first entry)
 DE Sequence of the VH region of monoclonal antibody PE1-1 against
 DE hepatitis B virus surface antigen.
 KW Hepatitis B virus; surface antigen; monoclonal antibody; therapy;
 KW HBsAg; diagnosis; HBV.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1...19
 FT /label= leader
 FT Region 20...117
 FT /label= VH III
 FT Region 50...54
 FT /label= CDR 1
 FT Region 69...85
 FT /label= CDR 2
 FT Region 118...129
 FT /label= D
 FT Region 130...143
 FT /label= JH 4
 PN WO9411495-A.
 PD 26-MAY-1994.
 PR 06-NOV-1992; U09749.
 PR 06-NOV-1992; WO-U09749.
 PA (SANO) SANDOZ LTD.
 PI Ostberg LG;
 DR WPI 94-183497/22.
 DR N-PSDB: Q64050.
 PT Monoclonal antibodies active against Hepatitis B surface antigen
 PT - for diagnosis and treatment of Hepatitis B virus
 PS Example; Page 35; 53pp; English.
 CC Human volunteers were immunised with hepatitis B vaccine. M13-4, ZM1-
 CC 2, ZM1-1 and PE1-1 hybridoma cell lines were derived from
 CC lymphocytes of individuals immunised with Heptavax (Merck & Co).
 CC Antibodies of PE1-1, ZM1-1, ZM1-2 and MD3-4 belong to the IgG1 class.
 CC The cell lines producing PE1-1, ZM1-1 and ZM1-2 were deposited as
 CC ATCC HB9234, 9191 and 9192 respectively. The cell lines all behave
 CC as typical (mouse x human) x human hybridomas and produce their
 CC respective Abs in concs. ranging up to 25 mg/l in standard
 CC suspension culture. The heavy variable (VH) and light variable (LH)
 CC chains of Abs PE1-1, ZM1-1, ZM1-2 and MD3-4 were isolated and
 CC sequenced. Total RNA was extracted from 10(7) hybridoma cells
 CC of each cell line. ss DNA was synthesised using AMV-reverse
 CC transcriptase and oligo-dT as primer. PCRs were performed and
 CC amplified DNA was size selected. ss DNA for sequencing was isolated
 CC from each positive clone after superinfection with M13K07.
 CC Sequencing was by the dideoxy chain termination method (Sanger
 CC et al.).
 SQ Sequence 143 AA;

Query Match 73.1%; Score 677; DB 9; Length 141;
 Best Local Similarity 76.6%; Pred. No. 1.57e-43;
 Matches 95; Conservative 11; Mismatches 14; Indels 4; Gaps 2;

DB 20 qvqlvesggvqpgsrslrslscasgftfrsrygmhwrqapqgkglewvavissdgsdyj 79
 QY 1 EVQLLESGGCVQPGSRSLRSLSCAASGFTFSAYGMHWRQAPQPGKGLWVAVIGWFGDSNOYY 60

MWRELF
(TN)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:03:05 1998; MasPar time 5.26 Seconds
504,498 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-4
Description: (1-125) from US08844215.pep
Perfect Score: 921
Sequence: 1 EVQLLESGGVGWPGGSLPL.....IKGRYLENNQGQILVTSS 125

Scoring table: PAM 150
Gap 11

Searched: 59021 seqs, 21210398 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11

Statistics: Mean 42.149; Variance 77.571; scale 0.543

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Prod. No.
1	583	74.2	122	5	HV3G_HUMAN IG HEAVY CHAIN V-III	9.64e-122
2	679	73.7	122	5	HV3H_HUMAN IG HEAVY CHAIN V-III	7.45e-121
3	636	69.1	125	5	HV3K_HUMAN IG HEAVY CHAIN V-III	2.50e-111
4	631	68.5	121	5	HV3L_HUMAN IG HEAVY CHAIN V-III	3.19e-110
5	596	64.7	119	5	HV3I_HUMAN IG HEAVY CHAIN V-III	1.67e-107
6	578	62.8	117	5	HV3C_HUMAN IG HEAVY CHAIN V-III	1.51e-98
7	578	62.8	120	5	HV3E_HUMAN IG HEAVY CHAIN V-III	1.51e-98
8	578	62.8	122	5	HV3A_HUMAN IG HEAVY CHAIN V-III	2.50e-98
9	577	62.6	119	5	HV3D_HUMAN IG HEAVY CHAIN V-III	1.78e-95
10	564	61.2	120	5	HV3F_HUMAN IG HEAVY CHAIN V-III	1.34e-94
11	560	60.8	116	5	HV3N_HUMAN IG HEAVY CHAIN V-III	6.08e-94
12	557	60.5	119	5	HV3M_HUMAN IG HEAVY CHAIN V-III	1.67e-93
13	555	60.3	116	5	HV3L_HUMAN IG HEAVY CHAIN V-III	9.37e-92
14	547	59.4	119	5	HV3M_HUMAN IG HEAVY CHAIN V-III	4.24e-91
15	544	58.2	115	5	HV3E_HUMAN IG HEAVY CHAIN V-III	2.37e-89
16	536	58.0	117	5	HV3D_HUMAN IG HEAVY CHAIN V-III	6.48e-89
17	534	58.0	114	5	HV3E_HUMAN IG HEAVY CHAIN V-III	3.60e-87
18	534	57.1	116	5	HV3D_HUMAN IG HEAVY CHAIN V-III	9.83e-87
19	526	57.1	116	5	HV3E_HUMAN IG HEAVY CHAIN V-III	4.42e-86
20	524	56.9	142	5	HV3L_HUMAN IG HEAVY CHAIN V-III	2.95e-85
21	521	56.6	97	5	HV56_MOUSE IG HEAVY CHAIN PRECUP	
22	515	55.9	117	5	HV55_MOUSE IG HEAVY CHAIN PRECUP	

FT	TURN	62	67
FT	STRAND	68	73
FT	TURN	74	77
FT	STRAND	78	83
FT	HELIX	88	90
FT	STRAND	92	99
FT	STRAND	106	106
FT	TURN	107	108
FT	STRAND	109	109
FT	STRAND	113	113
FT	STRAND	120	124
FSQ	SEQUENCE	126 AA; 13718 MW, 14F328CF CRC32;	

Query Match 69.1%; Score 636; DB 5; Length 126;
 Best Local Similarity 69.0%; Pred. No. 2.51e-111;
 Matches 87; Conservative 18; Mismatches 20; Indels 1; Gaps 1;

Db	1	qkvllvsgggvvgvqrsrlrlscsssqffissvaywrrqatgpgalewvaivwtdqsdguy	60
Qy	1	EVQLLEGGGVVQPGKSLRLSCAASGFTFKYGMHWVQAPGKGLEWVAGISFDGSNOYY	60
Db	61	adsvkgftrtdnsknrtllqmdslrpdetgvycardqdahfssasctqdywagst	120
Qy	61	ADSVKGRFIVSRDNRSDTVFLQMSLSRLIEDTAVYYCATEGSP-EGSIKGRYYLENWCGQT	119
Db	121	ptvysv 126	
Qy	120	LVTVSS 125	

RESULT 4
 ID HV31_HUMAN STANDARD, FRT: 121 AA.

AC	P01771;	
DT	21-JUL-1986 (PEL 01, CREATED)	
DT	21-JUL-1986 (REL 01, LAST SEQUENCE UPDATE)	
DT	21-JUL-1986 (REL 01, LAST ANNOTATION UPDATE)	
DE	IG HEAVY CHAIN V-III REGION (HIL).	
OS	HOMO SAPIENS (HUMAN).	
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
ON	EUTHERIA; PRIMATES.	
RC	[1]	
RP	SEQUENCE.	
RA	MEDLINE; 79124695.	
RR	CHIU Y.-Y.H., LOPEZ DE CASTRO J.A., POLJAK R.J.;	
RL	BIOCHEMISTRY 18:553-560(1979).	
RC	!- THIS CHAIN WAS ISOLATED FROM AN IgG1 MYELOMA PROTEIN.	
DR	PIR; A02054; G1HUHL.	
DR	HSSP; P01607; 1FGV.	
KW	IMMUNOGLOBULIN V REGION	
FT	MOD_RES 1 1	
FT	NON_TER 121 121	
FSQ	SEQUENCE 121 AA; 13566 MW, 8E91B7EC CRC32;	

Query Match 66.5%; Score 631; DB 5; Length 121;
 Best Local Similarity 66.4%; Pred. No. 2.16e-110;
 Matches 83; Conservative 20; Mismatches 18; Indels 4; Gaps 3;

Db	1	qkvllvsgggvvgvqrsrlrlscsssqffissvaywrrqatgpgalewvaivwtdqsdguy	60
Qy	1	EVQLLEGGGVVQPGKSLRLSCAASGFTFKYGMHWVQAPGKGLEWVAGISFDGSNOYY	60
Db	61	gdsvkgrftrtdnsknrtllqmdslrpdetgvycardqdahfssasctqdywagst	116
Qy	61	ADSVKGRFIVSRDNRSDTVFLQMSLSRLIEDTAVYYCATEGSP-EGSIKGRYYLENWCGQT	120
Db	117	vtvysv 121	
Qy	121	VTVSS 125	

RESULT 5
 ID HV31_HUMAN STANDARD; FRT: 119 AA.
 AC P01770;


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DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (NIE).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 77070269.
RA PONTING L., HILSCHMANN N.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1573-1604(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE; 77070267.
RA DREKER L., SCHWARZ J., PEICHEL W., HILSCHMANN N.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 357:1515-1540(1976).
CC -1- THIS CHAIN WAS ISOLATED FROM AN IGB1 MYELOMA PROTEIN.
DR PIR; A02053; GLHUNI.
DR HSSP; P01607; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT MOD.PES 1 1 PYRROLIDONE CARBOXYLIC ACID
FT DISULFID 22 96
FT NON-TER 119 119
SQ SEQUENCE 119 AA: 13242 MW: 5703CA8E CRC32:

Query Match 64.7%; Score 596; DB 5; Length 119,
Best Local Similarity 64.8%; Pred. No. 1,678-102;
Matches 81; Conservative 23; Mismatches 15; Indels 6; Gaps 4;

Db 1 qvqlvsgggvqvqgrslrlscasagffsrytlhwirgagpgkglewvavmsybgbbkhy 60
    |||||
QY 1 EVQLLESGGGVVQVQPSPSLRLSCAASGFFTKYTGMRHWVQAPGKGLEWVAGISFGSNQYY 60
    |||||

Db 61 adsvngrftisrndskntlylmnsrlrpdctavvyycari--r-dtam--ff-ahwgggtl 114
    |||||
QY 61 ADSVNGRFTIVSPNRPDTVFLQMSSRLPDTAVVYVCATEGSPFGSIKGRYYLENWGGTLL 120
    |||||

Db 115 vtvsx 119
    |||||
QY 121 VTVSS 125
    |||||

RESULT 6
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1984 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PFCFSPSP V-III REGION (VH26)
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81101090.
RA MATTHEYSENS G., RABBITTS T.H.;
RL PPOC NATL. ACAD. SCI. U.S.A. 77:6561-6565(1980).
DR EMBL; J00236; G553412;
DR EMBL; M35415; G553422;
DR PIR; A02047; H3H026.
DR HSSP; P01772; IIGM.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19 IG HEAVY CHAIN V-II REGION (VH26)
FT CHAIN 20 117
FT NON-TER 117 117
SQ SEQUENCE 117 AA: 12582 MW: 15A21B2A CRC32:

Query Match 62.8%; Score 578; DB 5; Length 117;
Best Local Similarity 77.3%; Pred. No. 1,51e-98;
Matches 75; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Db 20 evqllesggglvqpqgrslrlscasagffsrytmswvzqapqkglewvavmsybgbbkhy 70

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QY 1 EVQLLESGGGVVQVQPSPSLRLSCAASGFFTKYTGMRHWVQAPGKGLEWVAGISFGSNQYY 60
    |||||
Db 80 gdsykgfritsdskntlylmnsrlrpdctavvyycari--r-dtam--ff-ahwgggtl 116
    |||||
QY 61 ADSVNGRFTIVSPNRPDTVFLQMSSRLPDTAVVYVCATEGSPFGSIKGRYYLENWGGTLL 120
    |||||

RESULT 7
ID HV3C_HUMAN STANDARD; PRT; 120 AA.
AC P01766;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (BRO).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE; 77117674.
RA CAPPA J.D., HOPPE J.F.;
PL IMMUNOCHEMISTRY 13:995-999(1976)
CC -1- THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM THE SERUM OF A
    PATIENT WITH MALIGNANT LYMPHOMA OF THE WALDENSTROM TYPE.
DR PIR; A02049; M3HUBW.
DR HSSP; P01772; IFGV.
KW IMMUNOGLOBULIN V REGION.
FT MOD.PES 1 1 PYRROLIDONE CARBOXYLIC ACID
FT DISULFID 22 96
FT NON-TER 120 120
SQ SEQUENCE 120 AA: 13227 MW: B404C4F1 CRC32:

Query Match 62.8%; Score 578; DB 5; Length 120;
Best Local Similarity 65.9%; Pred. No. 1,51e-98;
Matches 81; Conservative 19; Mismatches 17; Indels 6; Gaps 4;

Db 1 evqllesggglvqpqgrslrlscasagffsrytmswvzqapqkglewvavmsybgbbkhy 59
    |||||
QY 1 EVQLLESGGGVVQVQPSPSLRLSCAASGFFTKYTGMRHWVQAPGKGLEWVAGISFGSNQYY 60
    |||||

Db 60 adsvkgfritsdskntlylmnsrlrpdctavvyycari--spyslvdgklyllyyysvsggg 117
    |||||
QY 61 ADSVKGFTIVSPNRPDTVFLQMSSRLPDTAVVYVCATEGSPFGSIKGRYYLENWGGTLL 117
    |||||

Db 118 gtl 120
    |||||
QY 118 GTL 120
    |||||

RESULT 8
ID HV3A_HUMAN STANDARD; PRT; 122 AA.
AC P01762;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (TRO).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE (MYELOMA PROTEIN TPO).
RX MEDLINE; 76023781.
RA KPATZIN H., ALTEVAGT P., PUGHAN F., KOPPT A., STAPOSCIR K.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 356:1337-1342(1975).
CC -1- THE SEQUENCE OF THE C REGION IS ALSO GIVEN.
DR PIR; A02045; A1HUTP.
DR HSSP; P01772; 8FAB.
KW IMMUNOGLOBULIN V REGION.
FT MOD.PES 1 1 PYRROLIDONE CARBOXYLIC ACID
FT NON-TER 122 122
SQ SEQUENCE 122 AA: 13472 MW: BF02D3E8 CRC32:

Query Match 62.9%; Score 579; DB 5; Length 122;

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Best Local Similarity 56.8%; Pred. No. 1,51e-98;
Matches 71; Conservative 29; Mismatches 22; Indels 3; Gaps 2;

Db 1 qvqlvsgggvlgkpggslriscvasgfsfrdfymwswirztpgkglzwsvyagsgstlyy 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGGGVQVQGRSLRLSCAASGFTFKTYGMHWROAPGKGLEWVAGISFDGSGNOYY 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 adsvkgrftisrdnaqkslylzmbslrbztbtavyycaatbb-fbw--stslbywqzqbl 117
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTVSRNSRDTVFLOMSS:PLEDTAVYYCATEGSPFGSIKGRYYLENWGQGTL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 118 vtvs 122
    :|||||
QY 121 VTSS 125

RESULT 9
ID HV3L HUMAN STANDARD: PRT: 119 AA.
AC P01773:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (BUR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE: 79151016.
RA PUTNAM F.W., LIU Y.-S.V., LOW T.T.K.;
RL J. BIOL. CHEM. 254:2865-2874(1979).
DR PIR: A02056; ALHUBR.
DR HSP: P01772; 1FGV.
KW IMMUNOGLOBULIN V REGION; GLYCOPROTEIN.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT CARBOHYD 28 28
FT NON_TER 119 119
SQ SEQUENCE 119 AA: 12981 MW; 323A4FE1 CRC32:

Query Match 62.6%; Score 577; DB 5; Length 119;
Best Local Similarity 63.7%; Pred No 2 50e-98;
Matches 79; Conservative 22; Mismatches 17; Indels 6; Gaps 2.

Db 1 qvqlvsgggvlgkpggslriscvasgfsfrdfymwswirztpgkglzwsvyagsgstlyy 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLESGGGVQVQGRSLRLSCAASGFTFKTYGMHWROAPGKGLEWVAGISFDGSGNOYY 60
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 adsvkgrftisrdnaqkslylzmbslrbztbtavyycaatbb-fbw--stslbywqzqbl 114
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTVSRNSRDTVFLOMSS:PLEDTAVYYCATEGSPFGSIKGRYYLENWGQGTL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 115 vtvs 118
    :|||||
QY 121 VTSS 124

RESULT 10
ID HV3L HUMAN STANDARD: PRT: 120 AA.
AC P01782:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (DOR).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 80020921.
RA STEINER L.A., GARCIA PARDO A., MARGOLIES M.N.;
RL BIOCHEMISTRY 18:4068-4080(1979).
RN [2]

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CRYSTALLIZATION.
PX MEDLINE: 80020920.
RA STEINER L.A., LOPES A.D.;
RL BIOCHEMISTRY 18:4054-4067(1979).
CC -1- THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION IN THE HINGE REGION.
CC THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN DISULFIDE BONDS.
DR PIR: A02065; GIHUBB.
DR HSP: P01789; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT NON_TER 120 120
SQ SEQUENCE 120 AA: 13440 MW; 100CF1CF CFC32:

Query Match 61.2%; Score 564; DB 5; Length 120;
Best Local Similarity 63.2%; Pred. No. 1,78e-95;
Matches 79; Conservative 21; Mismatches 20; Indels 5; Gaps 4;

Db 1 evqlvesggdlvqpqrslrlscasasfntfeynmhwlrqqpdkqpwvstltnuvsyly 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGGVQVQGRSLRLSCAASGFTFKTYGMHWVPAATKGLFWVAGISFDGSGNOYY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 adsvkgrfaisrdnaqklylqlnll:pedtatycaak-q--yiw-nauwfdswagqtl 115
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTVSRNSRDTVFLOMSS:PLEDTAVYYCATEGSPFGSIKGRYYLENWGQGTL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 116 vtvs 120
    :|||||
QY 121 VTSS 125

RESULT 11
ID HV3L HUMAN STANDARD: PRT: 116 AA.
AC P01781:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (GAL).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE.
RX MEDLINE: 75059123.
RA WATANABE S., RAZNIKOL H.U., HORN J., BERTRAM J., HILSCHMANN N.;
RL HOPPE-SEYLER'S Z. PHYSIOL. CHEM. 354:1505-1509(1973).
RN [2]
RP REVISION TO THE COMPOSITION OF 28-33.
RA HILSCHMANN N.;
RL SUBMITTED (JUN-1975) TO THE PIR DATA BANK.
CC -1- THIS MU CHAIN WAS ISOLATED FROM A WALDENSTROM'S MACROGLOBULIN.
DR PIR: A02064; M3HUGL.
DR HSP: P01607; 1FGV.
KW IMMUNOGLOBULIN V REGION.
FT NON_TER 116 116
SQ SEQUENCE 116 AA: 12730 MW; F112826C CFC32:

Query Match 60.8%; Score 560; DB 5; Length 116;
Best Local Similarity 67.2%; Pred No. 1,34e-94;
Matches 84; Conservative 16; Mismatches 14; Indels 9; Gaps 4;

Db 1 evqlvesggdlvqpqrslrlscasasfntfeynmhwlrqqpdkqpwvstltnuvsyly 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGGVQVQGRSLRLSCAASGFTFKTYGMHWVPAATKGLFWVAGISFDGSGNOYY 60
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 adsvkgrfaisrdnaqkslylqlnll:pedtatycaak-q--yiw-nauwfdswagqtl 111
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTVSRNSRDTVFLOMSS:PLEDTAVYYCATEGSPFGSIKGRYYLENWGQGTL 120
    :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 112 vtvs 116
    :|||||
QY 121 VTSS 125

RESULT 12

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ID  HV3M HUMAN          STANDARD:          PRT:  119 AA.
AC  P01775:
DT  21-JUL-1986 (REL. 01, CREATED)
DT  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT  21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE  IG HEAVY CHAIN V-III REGION (LAW).
OS  HOMO SAPIENS (HUMAN).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; PRIMATES.
RN  [1]
RP  SEQUENCE.
RX  MEDLINE: 75046755.
RA  CAPRA J.D., KEHOE J.M.; N S.A. 71:4032-4036(1974)
RL  PROC. NATL. ACAD. SCI.
CC  -!- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
CC  ACTIVITY.
DR  PIR: A02058; M3HUPM.
DR  HSSP: P01772; 1FGV.
KW  IMMUNOGLOBULIN V REGION.
FT  NON_TER  119
FT  SEQUENCE  119 AA; 12858 MW; 1CE0116C CRC32;
SQ

Query Match      60.5%; Score 557; DB 5; Length 119;
Best Local Similarity 59.0%; Pred. No. 6,08e-94;
Matches 72; Conservative 29; Mismatches 16; Indels 5; Gaps 4:

Db  2 vqllesgglyvpggslrlscaasftfssasmswrrcapkglewva-wkyengndkhy 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  2 vqllesgglyvpggslrlscaasftfssasmswrrcapkglewva-wkyengndkhy 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  61 adsvgrftisrdsnkntlylqmgqlqzavsaivycardagpy--vsptff-abwgggtl 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  61 adsvgrftisrdsnkntlylqmgqlqzavsaivycardagpy--vsptff-abwgggtl 117
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  118 vt 119
    ||
QY  121 vt 122

RESULT  13
ID  HV16 MOUSE          STANDARD:          PRT:  136 AA.
AC  P01783:
DT  21-JUL-1986 (REL. 01, CREATED)
DT  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT  01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE  IG HEAVY CHAIN PRECURSOR V REGION (MOPC 21) (FRAGMENT).
OS  MUS MUSCULUS (MOUSE).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
OC  EUTHERIA; RODENTIA.
RN  [1]
RP  SEQUENCE FROM N A.
RX  MEDLINE: 81234548.
RA  BOWTHWELL A.L.M., PASKIND M., PETH M., IMANISHI-KAPI T., PAJENSKY K.
RA  BALTIMORE D.;
RN  CELL 24:635-637(1991);
RN  [2]
RP  SEQUENCE OF 17-136
RX  MEDLINE: 77100368.
RA  ADEUGBO K., MILSTEIN C., SECHER D.S.;
RL  NATURE 265:299-304(1977).
DR  EMBL: J00522; G195055; -.
DR  PIR: A02066; G1MS21.
DR  HSSP: P01607; 1FGV.
KW  IMMUNOGLOBULIN V REGION; SIGNAL.
FT  NON_TER  1
FT  SIGNAL   <1 16
FT  CHAIN    17 136
FT  DOMAIN  115 119
FT  DOMAIN  120 136
FT  DISULFID 38 112
FT  NON_TER  136 136
FT  NON_TER  75 78
FT  CONFLICT 89 90
    HYAD -> DYAH (IN REF. 2)
    EN -> ND (IN REF. 2)

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FT  CONFLICT  115 115      W -> H (IN REF. 2).
FT  CONFLICT  120 120      Y -> K (IN REF. 2).
SQ  SEQUENCE  136 AA; 15071 MW; 24BFDEB8 CRC32;

Query Match      60.3%; Score 555; DB 5; Length 136;
Best Local Similarity 55.6%; Pred. No. 1.67e-93;
Matches 82; Conservative 20; Mismatches 18; Indels 5; Gaps 3:

Db  17 dvqlvesgglyvpggslrlscaasftfssasmswrrcapkglewva-wkyengndkhy 76
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  1  evqllesgglyvpggslrlscaasftfssasmswrrcapkglewva-wkyengndkhy 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  77 adtkerftisrdsnkntlylqmgqlqzavsaivycardagpy--vsptff-abwgggtl 131
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  61 adsvgrftisrdsnkntlylqmgqlqzavsaivycardagpy--vsptff-abwgggtl 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  132 vtss 136
    |||||
QY  121 vtss 125

RESULT  14
ID  HV3M HUMAN          STANDARD:          PRT:  119 AA.
AC  P01774:
DT  21-JUL-1986 (REL. 01, CREATED)
DT  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT  21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE  IG HEAVY CHAIN V-III REGION (POM)
OS  HOMO SAPIENS (HUMAN).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC  EUTHERIA; PRIMATES.
RN  [1]
RP  SEQUENCE.
RX  MEDLINE: 75046755.
RA  CAPRA J.D., KEHOE J.M.; N S.A. 71:4032-4036(1974)
FL  PROC. NATL. ACAD. SCI.
CC  -!- THIS CHAIN WAS ISOLATED FROM IGM WITH ANTI-GAMMA GLOBULIN
CC  ACTIVITY.
DR  PIR: A02057; M3HUPM.
DR  HSSP: P01772; 1FGV.
KW  IMMUNOGLOBULIN V REGION
FT  VARIANT   54  54
FT  NON_TER  119 119
FT  SEQUENCE  119 AA; 12953 MW; 2A5697D2 CRC32;
SQ

Query Match      55.4%; Score 547; DB 5; Length 119;
Best Local Similarity 53.3%; Pred. No. 9.37e-92;
Matches 73; Conservative 28; Mismatches 17; Indels 5; Gaps 4:

Db  1  evqllesgglyvpggslrlscaasftfssasmswrrcapkglewva-wkyengndkhy 59
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  1  evqllesgglyvpggslrlscaasftfssasmswrrcapkglewva-wkyengndkhy 59
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  60 yadvgrftisrdsnkntlylqmgqlqzavsaivycardagpy--vsptff-abwgggtl 116
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY  60 yadvgrftisrdsnkntlylqmgqlqzavsaivycardagpy--vsptff-abwgggtl 119
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db  117 lvt 119
    |||
QY  120 lvt 122

RESULT  15
ID  HV3E HUMAN          STANDARD:          PRT:  115 AA.
AC  P01767:
DT  21-JUL-1986 (REL. 01, CREATED)
DT  21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT  21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE  IG HEAVY CHAIN V-III REGION (BUT).
OS  HOMO SAPIENS (HUMAN).
OC  EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA.
OC  EUTHERIA; PRIMATES.

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Thu Feb 26 07:06:04 1998

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RN  SEQUENCE.
RP  MEDLINE: 78137069.
RX  TORANO A.; PUTNAM F.W.;
RA  PROC. NATL. ACAD. SCI. U.S.A. 75:966-969(1978).
RL  CC -!- THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C REGION OF THIS
CC  MYELOMA PROTEIN IS ALSO GIVEN.
DR  PIR: A02050; A2HUBU.
DR  HSP: P01772; IFGV.
KW  IMMUNOGLOBULIN V REGION.
FT  NON_TER 115 115
SQ  SEQUENCE 115 AA: 12379 MW: 90803472 CPC32;

Query Match      59.1%; Score 544; DB 5; Length 115;
Best Local Similarity 69.7%; Pred. No. 4.24e-91;
Matches 69; Conservative 17; Mismatches 12; Indels 1; Gaps 1;

Db      1  evqlvetgggllqpqgsrlscaasgflvsbhmswvrgqpgkalzwwsai-yrgattvy 59
QY      1  EVQLLESGGGVVQPGKSLRLSCAASGFTFKTYGMHWVRQAPGKLEWVAGISFDGSNQYY 60

Db      60  adsvkgrftisrddrbtvyqlmbslraedtavyyycard 98
QY      1  ADSVKGRFIVSRDNRDVFVFLQMSSLRLIEDTAVYYCATE 99

Search completed: Tue Feb 24 07:09:20 1998
Job time : 15 secs.

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Db 480 adsvkgrftisrdsnkntlfqlmshlraadtovyyvcaakdqlyfsgsqspghy---wvqgtl 136
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 vtvt 140
QY 120 VTVS 123

RESULT 13
ID R50315 standard; Protein: 122 AA.
AC R50315;
DT 05-OCT-1994 (first entry)
DE Humanised heavy chain variable region Pfzhlc2-6.
KW Monoclonal antibody, Plasmodium falciparum, CDR;
KW Complementarity determining region; fusion protein;
KW murine, variable; light; heavy; chain, malaria.
OS Synthetic.
FH Key Location/Qualifiers
FT Misc_difference 49
FT /note="
FT WO9405690-A.
PD 17-MAR-1994.
PR 08-SEP-1993; U08435.
PR 09-SEP-1992; US-941654.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (USNA ) US SEC OF ARMY.
PA (USNA ) US SEC OF NAVY.
PI Charoenvit Y, Hoffman S, Hurle M, Rosenberg M;
PI Sadoff JC, Sylvester DR, Gross MS;
DR WPI: 94-101115/12.
DR N-PSDB: Q44840.
PT New engineered antibodies and fusion proteins for preventing
PT Plasmodium infection - contg. murine antibody CDR sequences, and
PT corresp. nucleic acid, vectors and transformed cells
PS Claim 14; Fig 9; 98pp; English.
CC Example 4 describes the prodn. of a high affinity humanised
CC antibody. At amino acid position 49, the Ser of the humanised
CC heavy chain Pfzhlc2-3 was changed to Ala, which is the amino
CC acid found at this position in the native murine NSF2.
SQ Sequence 122 AA.

Query Match 72.8%; Score 674; DB 9; Length 122;
Best Local Similarity 75.0%; Pred. No. 2.72e-43;
Matches 93; Conservative 14; Mismatches 15; Indels 2; Gaps 2;

Db 1 evqllesggglvqpgsgslrlscaasgftfssvamsvrrqapkglewraeisdgsgsty 60
QY 1 EVOLLESGGGVVQPGSRLSLCAASGFTFSAYGMHWVRQAPKGLWVAGWFGDSNQYY 60

Db 61 pdtvtgrftisrdsnkntlfqlmshlraadtavyycasliyyg-ydg-yandywqggtlv 118
QY :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 SDSVKGPFVSPDNPNTLFLQWNSLPPEDTAVYYCATEVLFGSIKGPYYLENWGQGTTLV 120
QY :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 119 tvss 122
QY 121 TVSS 124

RESULT 14
ID R54784 standard; peptide: 125 AA.
AC R54784;
DT 18-OCT-1994 (first entry)
DE SpA-reactive IgM heavy chain clone 18/2.
KW SpA domain D; Ig binding region; IgM; B-cell superantigen; sAg;
KW Superantigen, heavy chain variable region; VH3 restricted antibody;
KW VH; protein-A; B-lymphocyte; vaccine.
OS Homo sapiens.
PN WO9409818-A.
PD 11-MAY-1994.
PR 29-OCT-1993; U10555.
PR 30-OCT-1992; US-969936.
PA (REGC ) UNIV CALIFORNIA.

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PI Silverman GJ;
DR WPI: 94-167127/20.
PT Stimulating prodn. of variable region gene family restricted
PT antibodies - through B-cell super-antigen vaccination
PS Disclosure: Page 66; 130pp; English
CC A B-cell superantigen (sAg) is a fragment of SpA D domain that
CC specifically binds the Fab portion of variable region restricted
CC antibodies. The sAg is used to enhance production of VH, especially
CC VH3, restricted Abs. During attempts to identify sAg, aa sequences
CC (R54784-801) of H chains from Ig reactive with mod-SpA, and aa and
CC DNA sequences (P54802-16, C64942-56) of VH regions of SpA binders
CC obtained from combinatorial libraries were determined. IgM
CC protein 18/2 derives from the germline configuration of VH gene
CC segments.
SQ Sequence 125 AA.

Query Match 72.7%; Score 673; DB 9; Length 125;
Best Local Similarity 73.8%; Pred. No. 3.26e-43;
Matches 93; Conservative 17; Mismatches 13; Indels 3; Gaps 3;

Db 1 evqllesggglvqpgsgslrlscaasgftfssvamsvrrqapkglewraeisdgsgsty 60
QY 1 EVOLLESGGGVVQPGSRLSLCAASGFTFSAYGMHWVRQAPKGLWVAGWFGDSNQYY 60

Db 61 adsvkgrftisrdsnkntlfqlmshlraadtavyytkqqlviyyg-sgsyhwfdpwggt 119
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SDSVKGPFVSPDNPNTLFLQWNSLPPEDTAVYYCAT-EVIFGSIKGPYY-LENWGQGT 118
Db 120 ltvss 125
QY 119 LTVSS 124

RESULT 15
ID R50312 standard; Protein: 122 AA.
AC R50312;
DT 05-OCT-1994 (first entry)
DE Humanised heavy chain variable region Pfzhlc2-3.
KW Monoclonal antibody; plasmodium falciparum; CDR;
KW Complementarity determining region; fusion protein;
KW murine; variable; light; heavy; chain; malaria.
OS Synthetic.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50..56
FT /label= CDR2
FT Region 99..111
FT /label= CDR3
FT WO9405690-A.
PD 17-MAR-1994.
PR 08-SEP-1993; U08435.
PR 09-SEP-1992; US-941654.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (USNA ) US SEC OF ARMY.
PA (USNA ) US SEC OF NAVY.
PI Charoenvit Y, Hoffman S, Hurle M, Rosenberg M;
PI Sadoff JC, Sylvester DR, Gross MS;
DR WPI: 94-101115/12.
DR N-PSDB: Q44826.
PT New engineered antibodies and fusion proteins for preventing
PT Plasmodium infection - contg. murine antibody CDR sequences, and
PT corresp. nucleic acid, vectors and transformed cells
PS Claim 5; Fig 6; 98pp; English.
CC Naturally-occurring (Q44841-42) and synthetic (Q44825-28)
CC variable light chain and variable heavy chain sequences
CC derived from murine mAb NFS2 are provided. Murine mAb NFS2,
CC its variable chain peptides, CDRs, functional fragments,
CC Fab fragments, and analogs are useful in prodn. of fusion
CC proteins, esp. engineered antibodies. These prods. are
CC used to protect humans against Plasmodium infections.
SQ Sequence 122 AA.

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Query Match      72.6%; Score 672; DB 9; Length 122;
Best Local Similarity 74.2%; Pred. NO. 3.92e-43;
Matches 92; Conservative 15; Mismatches 15; Indels 2; Gaps 2;

Db 1 evqllesggglvqpqgsrlrlscaasgftfssyamswwrqapqkglewvseisdagsytyy 60
QY 1 EVOLLESGGGVVQPGRSLRLSCAASGFTFSAYGMHWVRQAPKGLEWVAGIWFDDGSNQYY 60

Db 61 pdtvtgrftisrdnsknltlylqmnslraedtavvyacasliyyg-ydq-yandywaggtlv 118
QY 61 SDSVKGRFTVSPDNRNTLFLQMNSLRPEDTAVVYVCATEVLFGSIKQPYYLENMWQGTIV 120

Db 119 tvss 122
QY 121 TVSS 124

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Search completed: Tue Feb 24 07:13:04 1998
Job time : 33 secs.

WQESRLH (TM)

Release 2.1b John F. Collins, Biocomputing Research Unit,
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:04:38 1998; MasPar time 9.04 seconds
383.249 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-4

Description: (1-125) from US08844215.pep

Perfect Score: 921

Sequence: 1 EVOLLEGGGVQPGPSLPL.....IKGPYLENNWGGTILVTSS 125

Scoring table: PAM 150

Gap 11

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: pir53

1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3

8:unann4 9:unann5 10:unann6 11:unann7 12:unann8

13:unann9 14:unann10 15:unann11 16:unann12 17:unann

18:unrev

Statistics: Mean 41.619; Variance 120.293; scale 0.346

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	701	76	121	7	Ig heavy chain V reg	2.39e-79
2	686	74.5	151	7	Ig heavy chain precu	3.22e-77
3	684	74.3	122	7	Ig heavy chain - hum	6.18e-77
4	683	74.2	122	2	Ig heavy chain V-III	8.57e-77
5	680	73.8	122	2	Ig heavy chain V-III	2.28e-76
6	679	73.7	122	2	Ig heavy chain V-III	3.16e-76
7	677	73.5	120	7	Ig heavy chain V reg	6.07e-76
8	672	73.0	128	7	Ig heavy chain V reg	3.10e-75
9	670	72.7	118	7	Ig heavy chain - hum	5.96e-75
10	670	72.7	121	7	Ig heavy chain V reg	5.96e-75
11	670	72.7	139	7	Ig heavy chain V reg	5.96e-75
12	664	72.1	123	7	Ig heavy chain - hum	4.21e-74
13	663	72.0	133	7	Ig heavy chain V-III	5.83e-74
14	662	71.9	132	7	Ig heavy chain V reg	8.08e-74
15	661	71.8	120	7	Ig heavy chain - hum	1.12e-73
16	661	71.8	133	7	Ig heavy chain - hum	1.12e-73
17	658	71.4	119	7	Ig mu chain - human	2.97e-73
18	650	70.6	119	7	Ig heavy chain V reg	4.02e-72
19	650	70.6	127	7	Ig heavy chain V reg	4.02e-72
20	650	70.6	125	7	Ig heavy chain V reg	4.02e-72

21	559	70.6	160	7	S05271	Ig heavy chain precu	4.02e-72
22	548	70.4	122	7	S31112	Ig heavy chain - hum	7.71e-72
23	547	70.2	124	7	S20782	Ig heavy chain V reg	1.07e-71
24	545	70.0	111	7	PH1643	Ig heavy chain V reg	2.05e-71
25	545	70.0	120	7	S44111	Ig heavy chain V-D-J	2.05e-71
26	544	69.9	123	7	S30532	Ig heavy chain V reg	2.83e-71
27	543	69.8	123	7	S31114	Ig heavy chain - hum	3.92e-71
28	543	69.8	127	7	S38489	Ig heavy chain - hum	3.92e-71
29	540	69.5	117	7	S36259	Ig heavy chain V reg	1.04e-70
30	540	69.5	140	7	S31588	Ig heavy chain V reg	1.04e-70
31	539	69.4	121	7	I55673	IgM - human (fragmen	1.44e-70
32	538	69.3	119	7	S31107	Ig heavy chain - hum	1.99e-70
33	538	69.3	121	7	S31104	Ig heavy chain (subc	1.99e-70
34	538	69.3	127	7	S31701	Ig heavy chain V reg	1.99e-70
35	537	69.2	147	7	I37780	Ig variable region (2.76e-70
36	536	69.1	126	2	GIHUKL	Ig heavy chain V-III	3.82e-70
37	536	69.1	140	7	S31686	Ig heavy chain V reg	3.82e-70
38	535	68.9	120	7	S36273	Ig heavy chain V reg	5.29e-70
39	535	68.9	122	7	S69910	Ig V-D-J region (KR	5.29e-70
40	534	68.8	98	7	PL0116	Ig heavy chain V-III	7.32e-70
41	524	68.9	114	7	S46390	Ig heavy chain V reg	7.32e-70
42	534	68.8	141	7	S31569	Ig heavy chain V reg	7.32e-70
43	533	68.7	134	7	S31679	Ig heavy chain V reg	1.01e-69
44	531	68.5	113	7	S38490	Ig heavy chain - hum	1.94e-69
45	531	68.5	121	2	GIH7HL	Ig heavy chain V-III	1.94e-69

ALIGNMENTS

RESULT 1

ENTRY

TITLE

ORGANISM

DATE

ACCESSIONS

REFERENCE

#authors

#journal

#title

#cross-references

#accession

##molecule_type

##residues

##cross-references

CLASSIFICATION

KEYWORDS

FEATURE

SUMMARY

Query Match

Best Local Similarity

Matches

Db

Qy

Db

Qy

Db

Qy

RESULT 2

ENTRY

TITLE

```

ORGANISM      #formal_name Homo sapiens #common_name man
DATE          31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
              16-Aug-1996
ACCESSIONS    A60943; A48165
REFERENCE     Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.;
              Alt, F.W.; Kabat, E.A.; Latov, N.
#authors      J. Neuroimmunol. (1990) 30:245
#journal      Molecular cloning of a human immunoglobulin heavy chain
#title        variable (V-H) region with anti-myelin-associated
              glycoprotein activity.
#accession    A60943
#status       not compared with conceptual translation
#molecule_type mRNA
#residues     1-151 #label DES
REFERENCE     Desai, R.; Spatz, L.; Matsuda, T.; Ilyas, A.A.; Berman, J.E.;
              Alt, F.W.; Kabat, E.A.; Latov, N.
#authors      J. Neuroimmunol. (1990) 26:35-41
#journal      Molecular cloning of a human immunoglobulin heavy chain
#title        variable (V-H) region with anti-myelin-associated
              glycoprotein activity.
#accession    A48165
#molecule_type mRNA
#residues     1-36, 'M', 38-62, 'AR', 67-151 #label DE2
#note         this sequence has been corrected in reference A60943
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        34-117
SUMMARY        #domain immunoglobulin homology #label IMM
              #length 151 #molecular-weight 16212 #checksum 3341
Query Match   74.5%; Score 686; DB 7; Length 151;
Best Local Similarity 72.8%; Pred. No. 3,22e-77;
Matches 91; Conservative 16; Mismatches 17; Indels 1; Gaps 1,

Db 20 qvllvesggvqpqlrlscasqftfssygmhwvrgqpggglewvsvifdggtkyy 79
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Qy 1 EVQLLESGGVPVQPSRLSLSCASQFTFKTYGMHWVROAPKGLIEWVAGISFDGSSNOYY 60
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Db 80 advskgrftisrdnsntlylqmslracdtavvyvcard-f-fappn-wshidywqgtl 138
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Qy 61 ADSVKGPFIWSPNPTVFIQMSLSLEDTAVVYCATGSPSPGSIKGPYYIENWQGTTL 120
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Db 139 vtysl 143
   : :::::
Qy 121 VTVSS 125

RESULT 3
ENTRY     S31117 #type complete
TITLE     Ig heavy chain - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      02-Dec-1993 #sequence_revision 26-May-1996 #text_change
              16-Aug-1996
ACCESSIONS S31117
REFERENCE   Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol,
              M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
#authors    Eur. J. Immunol. (1992) 22:247-251
#journal    Restricted utilization of germ-line V(H)3 genes and short
              diverse third complementarity-determining regions (CDR3) in
              human fetal B lymphocyte immunoglobulin heavy chain
              rearrangements.
#accession  S31117
#status     preliminary; nucleic acid sequence not shown.
              translation not shown
#molecule_type mRNA
#residues   1-122 #label RAA
#cross-references EMBL:X62967
#note         the nucleotide sequence was submitted to the EMBL Data
              Library, October 1991
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

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heterotetramer; immunoglobulin
KEYWORDS      #domain immunoglobulin homology #label IMM
FEATURE       #length 122 #molecular-weight 13664 #checksum 8348
SUMMARY
Query Match   74.3%; Score 684; DB 7; Length 122;
Best Local Similarity 74.4%; Pred. No. 6,18e-77;
Matches 93; Conservative 17; Mismatches 12; Indels 3; Gaps 3;

Db 1 qvllvesggvqpqlrlscasqftfssygmhwvrgqpggglewvsvifdggtkyy 60
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Qy 1 EVQLLESGGVPVQPSRLSLSCASQFTFKTYGMHWVROAPKGLIEWVAGISFDGSSNOYY 60
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Db 61 advskgrftisrdnsntlylqmslracdtavvyvcard-f-fappn-wshidywqgtl 117
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Qy 61 ADSVKGRFIVSRDNRDTVFIQMSLSLEDTAVVYCATGSPSPGSIKGPYYIENWQGTTL 120
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Db 118 vtysl 122
   : :::::
Qy 121 VTVSS 125

RESULT 4
ENTRY     M3HUAM #type complete
TITLE     Ig heavy chain V-III region (Cam) - human
ORGANISM  #formal_name Homo sapiens #common_name man
DATE      31-Aug-1980 #sequence_revision 23-Oct-1981 #text_change
              31-Mar-1997
ACCESSIONS A02051
REFERENCE   Lehman, D.W.; Putnam, F.W.
              Proc. Natl. Acad. Sci. U.S.A. (1980) 77:3249-3244
#authors    Amino acid sequence of the variable region of a human mu
              chain; location of a possible J-H segment.
#title
#cross-references MIM:81013859
#accession  A02051
#molecule_type protein
#residues   1-122 #label IEH
COMMENT     This mu chain was isolated from the plasma of a patient with
              macroglobulinemia.
GENETICS    GDB:IGHV#
#gene
#cross-references GDB:128528
#map_position 14q32.33-14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin; pyroglutamic acid
FEATURE        15-98
              1
SUMMARY       #domain immunoglobulin homology #label IMM
              #modified_site pyrrolidone carboxylic acid (Gln) #status
              experimental
              #disulfide_bonds #status predicted
              #length 122 #molecular-weight 13668 #checksum 7281
Query Match   74.2%; Score 683; DB 2; Length 122;
Best Local Similarity 67.2%; Pred. No. 8,57e-77;
Matches 84; Conservative 27; Mismatches 11; Indels 3; Gaps 2;

Db 1 qvllvesggvqpqlrlscasqftfssygmhwvrgqpggglewvsvifdggtkyy 60
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Qy 1 EVQLLESGGVPVQPSRLSLSCASQFTFKTYGMHWVROAPKGLIEWVAGISFDGSSNOYY 60
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Db 61 advskgrftisrdnsntlylqmslracdtavvyvcard-f-fappn-wshidywqgtl 117
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
Qy 61 ADSVKGPFIWSPNPTVFIQMSLSLEDTAVVYCATGSPSPGSIKGPYYIENWQGTTL 120
   : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::

Db 118 vtysl 122
   : :::::
Qy 121 VTVSS 125

RESULT 5
ENTRY     E36005 #type complete
TITLE     Ig heavy chain V region (M77) - human

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ORGANISM      #formal_name Homo sapiens #common_name man
DATE          21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
ACCESSIONS    E36005
REFERENCE      A36005
#authors      Schroeder Jr., H.W.; Wang, J.Y.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150
#title        Preferential utilization of conserved immunoglobulin heavy
              chain variable gene segments during human fetal life.
#cross-references MUID:90349571
#accession    E36005
##status      preliminary
##molecule_type mRNA
##residues    1-122 ##label SCH
##cross-references GB:M34030
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        15-98
SUMMARY        #domain immunoglobulin homology #label IMM
              #length 122 #molecular-weight 13527 #checksum 530
Query Match    73.8%; Score 680; DB 7; Length 122;
Best Local Similarity 74.6%; Pred. No. 2.28e-76;
Matches 94; Conservative 17; Mismatches 10; Indels 5; Gaps 4;
Db 1 qvqlvsgggvvpqrsirlscasgffsfssyhmhwraqpqlgiewvavlsydgsknyy 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGTVVQPGPSLPISCAASGFTFKYGMHWVPQAPGKGFVWAGTSPFGSNQYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 adsvkrftiarnskntlylqmslraedtavvycard-rh-ss--swyygmdivwgggt 116
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ADSVKGPFIVSPDNGPTVFLQMSLPLEDTAVVYCATGSPFGSIKGPYY-LENWQGT 119
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 117 tvtvs 122
   :|||||
QY 120 LTVSS 125
   :|||||

RESULT 6
ENTRY    M1HMGCA #type complete
TITLE    Ig heavy chain V-III region (Ga) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     #sequence_revision 23-Oct-1981 #text_change 31-Dec-1996
ACCESSIONS A02052
REFERENCE   Florent, G.; Lehman, D.; Putnam, F.W.
#authors    Biochemistry (1974) 13:2482-2490
#journal     The switch point in mu heavy chains of human IgM
#title       immunoglobulins.
#cross-references MUID:74175307
#accession  A02052
##molecule_type protein
##residues  1-122 ##label FLO
COMMENT     This chain was isolated from a Waldenström's macroglobulin.
GENETICS
#gene       GDB:IGHV6
#cross-references GDB:128528
#map_position 14q32.33-14q32.33
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin, pyroglytamic acid
FEATURE        15-98
SUMMARY        #domain immunoglobulin homology #label IMM
              #modified_site pyrrolidone carboxylic acid (Gln) #status
              experimental
              #disulfide_bonds #status predicted
              #length 122 #molecular-weight 13166 #checksum 7775
Query Match    73.7%; Score 679; DB 2; Length 122;
Best Local Similarity 64.0%; Pred. No. 3.16e-76;
Matches 80; Conservative 30; Mismatches 12; Indels 3; Gaps 1;
Db 1 qvqlvsgggvvpqrsirlscasgffsfssyhmhwraqpqlgiewvavlsydgbbzyy 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

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QY 1 EVQLLESGGTVVQPGPSLPISCAASGFTFKYGMHWVPQAPGKGFVWAGTSPFGSNQYY 60
Db 61 adsvkrftiarnskntlylqmslraedtavvycard-rh-ss--swyygmdivwgggt 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ADSVKGPFIVSPDNGPTVFLQMSLPLEDTAVVYCATGSPFGSIKGPYY-LENWQGT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 118 vtiss 122
   :|||||
QY 121 VTSS 125
   :|||||

RESULT 7
ENTRY    S36278 #type fragment
TITLE    Ig heavy chain V region (clone alpha-TU-23) - human
              (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
              16-Aug-1996
ACCESSIONS S36278
REFERENCE   Griffiths, A.D.; Walevski, M.; Marks, J.D.; Rye, J.M.;
#authors    Embleton, M.J.; McGafferty, J.; Baier, M.; Holliger, K.P.;
              Gorick, R.D.; Hughes-Jones, N.C.; Hoogenboom, H.P.; Winter,
              G.
#journal     EMBO J. (1993) 12:725-734
#title       Human anti-self antibodies with high specificity from phage
              display libraries.
#accession  S36278
##status    preliminary; nucleic acid sequence not shown
##molecule_type mRNA
##residues  1-120 ##label GPI
##cross-references EMBL:Z18430
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        15-98
SUMMARY        #domain immunoglobulin homology #label IMM
              #length 120 #checksum 7337
Query Match    73.5%; Score 677; DB 7; Length 120;
Best Local Similarity 72.6%; Pred. No. 6.07e-76;
Matches 90; Conservative 19; Mismatches 11; Indels 4; Gaps 4;
Db 1 qvqlvsgggvvpqrsirlscasgffsfssyhmhwraqpqlgiewvavlsydgbbzyy 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 EVQLLESGGTVVQPGPSLPISCAASGFTFKYGMHWVPQAPGKGFVWAGTSPFGSNQYY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 adsvkrftiarnskntlylqmslraedtavvycard-rh-ss--swyygmdivwgggt 116
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 ADSVKGPFIVSPDNGPTVFLQMSLPLEDTAVVYCATGSPFGSIKGPYY-LENWQGT 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 117 vtvs 120
   :|||||
QY 121 VTSS 124
   :|||||

RESULT 8
ENTRY    S48797 #type complete
TITLE    Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human
              (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE     13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
              16-Aug-1996
ACCESSIONS S48797
REFERENCE   Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
#authors    Submitted to the EMBL Data Library.
#title       Molecular characterization of natural human anti-Sm
              autoantibodies.
#accession  S48797
##status    preliminary
##molecule_type mRNA
##residues  1-128 ##label MAH
##cross-references EMBL:Z46379
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology

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16-Aug-1996
G36005
A36005
Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6146-6150
Preferential utilization of conserved immunoglobulin heavy
chain variable gene segments during human fetal life.
#cross-references MUID:90349571
#accession G36005
#status preliminary
#molecule_type mRNA
#residues 1-121 #label SCH
#cross-references GB:M34031
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-96 #domain immunoglobulin homology #label IMM
SUMMARY
#length 121 #molecular-weight 13508 #checksum 6962

Query Match 72.7%; Score 670; DB 7; Length 121;
Best Local Similarity 74.4%; Pred. No. 5,96e-75;
Matches 93; Conservative 15; Mismatches 13; Indels 4; Gaps 3;

Db 1 qvqlvesggvqpgsrslrscasgftsfssygmhwvraqpdkglewaviydgskyy 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGVPQGRSLPLSCAASGFTFTYGMHWVRQAPGKLEWVAGISFDGSNQY 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 adsvkgrftisrdnsknltlylqmslraedtavvyccardkdwg--a-ll-dywaqql 116
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTIVSRDNRDITVFLQMSRLREDAVYVCATEGSPFGSIKGRYYLENWGQ 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 117 vtvs 121
|||||
QY 121 VTVSS 125

RESULT 11
ENTRY Ig heavy chain V region - human (fragment)
TITLE #formal_name Homo sapiens #common_name man
ORGANISM 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change
DATE 16-Aug-1996
ACCESSIONS S31674
REFERENCE S31585
#authors Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Pouquerrou, M.;
Tonnelle, C.
#submission Submitted to the EMBL Data Library, June 1992
#description Mechanisms that generate human immunoglobulin diversity
Operate from the 8th week of gestation in fetal liver.
#accession S31674
#status preliminary
#molecule_type mRNA
#residues 1-139 #label CUI
#cross-references EMBL:214204
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
34-117 #domain immunoglobulin homology #label IMM
SUMMARY
#length 139 #checksum 3756

Query Match 72.7%; Score 670; DB 7; Length 139;
Best Local Similarity 75.2%; Pred. No. 5,96e-75;
Matches 94; Conservative 15; Mismatches 11; Indels 5; Gaps 3;

Db 20 qvqlvesggvqpgsrslrscasgftsfssygmhwvraqpdkglewaviydgskyy 79
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVQLLESGGVPQGRSLPLSCAASGFTFTYGMHWVRQAPGKLEWVAGISFDGSNQY 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 adsvkgrftisrdnsknltlylqmslraedtavvyccakqlaf--fn-wl--dpwaqql 134
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 ADSVKGRFTIVSRDNRDITVFLQMSRLREDAVYVCATEGSPFGSIKGRYYLENWGQ 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 135 vtvs 139

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```

QY 121 VTSS 125
|||||
RESULT 12
ENTRY S38493 #type fragment
TITLE Ig heavy chain - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
16-Aug-1995
ACCESSIONS S38493
REFERENCE S38498
#authors Marks, J.D.; Guehand, W.H.; Bye, J.M.; Finnern, R.; Gorick,
B.D.; Voak, D.; Thorpe, S.; Hughes-Jones, N.C.; Winter, G.
#submission submitted to the EMBL Data Library, June 1993
#description Human antibody fragments specific for human blood group
antigens from a phage display library.
#accession S38493
#status preliminary
#molecule_type DNA
#residues 1-123 #label MAP
#cross-references EMBL:Z23036
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 123 #checksum 2856

Query Match 72.0%; Score 664; DB 7; Length 123;
Best Local Similarity 73.0%; Pred. No. 4.21e-74;
Matches 92; Conservative 12; Mismatches 19; Indels 2; Gaps 1;

Db 1 qvqlsgggvvgpgrslrslcaasgftfssygmhvwrgapkglewavvisydgskny 60
|||||
QY 1 EVQLLESGGAVGQPRSLRSLCAASGFTFKTYGMHWVPAPKGLFWASISFTSSNAYY 60
|||||

Db 61 adsvkgrftisrdnsktllylqmslraedtavvycaard-rll-tlaaagnfdywggtl 118
|||||
QY 61 ADSVKGRFIVSPNSPTVFLQMSLRLDTAVVYCATESPPGSIKGYLYLENWQGGTL 120
|||||

Db 119 vtss 123
|||||
QY 121 VTSS 125
|||||

RESULT 14
ENTRY S31603 #type complete
TITLE Ig heavy chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change
16-Aug-1996
ACCESSIONS S31603
REFERENCE S31585
#authors Cuisinier, A.M.; Gauthier, L.; Roubli, L.; Fougerean, M.;
Tonnelle, C.
#submission submitted to the EMBL Data Library, June 1992
#description Mechanisms that generate human immunoglobulin diversity
Operate from the 8th week of gestation in fetal liver.
#accession S31603
#status preliminary
#molecule_type mRNA
#residues 1-132 #label CUI
#cross-references EMBL:Z14168
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 30-113
SUMMARY #domain immunoglobulin homology #label IMM
#length 132 #molecular_weight 4666 #checksum 8700

Query Match 71.9%; Score 662; DB 7; Length 132;
Best Local Similarity 76.0%; Pred. No. 8.08e-74;
Matches 95; Conservative 14; Mismatches 8; Indels 8; Gaps 2;

Db 16 qvqlsgggvvgpgrslrslcaasgftfssygmhvwrgapkglewavvisydgskny 75
|||||
QY 1 EVQLLESGGAVGQPRSLRSLCAASGFTFKTYGMHWVPAPKGLFWASISFTSSNAYY 60
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Db 76 adsvkgrftisrdnsktllylqmslraedtavvycaard-rf-----yyfdywggtl 127
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QY 61 ADSVKGRFIVSPNSPTVFLQMSLRLDTAVVYCATESPPGSIKGYLYLENWQGGTL 120
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Db 129 vtss 132
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QY 121 VTSS 125
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RESULT 15
ENTRY S31112 #type complete
TITLE Ig heavy chain - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 02-Dec-1993 #sequence_revision 26-May-1995 #text_change
16-Aug-1996
ACCESSIONS S31112
REFERENCE S31104
#authors Paaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol,
M.J.D.; Vossen, J.M.; Schuurman, R.K.B.
#journal Eur. J. Immunol. (1993) 23:247-251
#title Restricted utilization of germ-line V(H)3 genes and short
diverse third complementarity-determining regions (CDR3) in
human fetal B lymphocyte immunoglobulin heavy chain

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#accession S31112 rearrangements.
#status preliminary; nucleic acid sequence not shown;
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#note the nucleotide sequence was submitted to the EMBL Data
Library, October 1991
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KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 120 #molecular-weight 12974 #checksum 8808

Query Match 71.8%; Score 661; DB 7; Length 120;
Best Local Similarity 76.0%; Pred No 1 12e-73;
Matches 95; Conservative 13; Mismatches 12; Indels 5; Gaps 3;

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1 EVQLLESGGCVVQPGKSLRLSCAASGFTFTKTYGMHWVRQAPGKLEWVAGISFDGSNQYY 60

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61 ADSVKGFIVSPDNRSDTVFIQMSSLRLEDTAIVYCATGSPFGSIKGRYYLENWQGGIL 120

Db 116 vtvss 120
QY :|||||
121 VTVSS 125

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Search completed: Tue Feb 24 07:09:52 1998
Job time : 14 secs.

WORLD
***** (TM)

Release 2 ID John F. Collins, BioComputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:37:11 1998; Master time 2.42 Seconds
Tabular output not generated. 186.065 Million cell updates/sec

Title: >US-08-844-215-4
Description: (1-125) from US08844215.pep
Perfect Score: 921
Sequence: 1 EVQLLESGGCVGQGRSLRL IKGPYYLENWGGITLVSS 125

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:58 10:59
10:PC192 11:PC193 12:PC194 13:PC195 14:PC196

Statistics: Mean 28.138; Variance 145.429; scale 0.193

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No
1	669	72.3	119	7	US-08-331- Sequence 46, Applicat	1.80e-44
2	665	72.3	120	7	US-07-942- Sequence 35, Applicat	2.15e-44
3	657	71.3	141	6	US-08-259- Sequence 2, Applicatio	1.70e-43
4	652	71.3	141	7	US-08-468- Sequence 2, Applicatio	1.70e-43
5	652	70.8	125	7	US-08-478- Sequence 99, Applicati	4.32e-43
6	650	70.6	125	11	PCT-US93-1 Sequence 5, Applicatio	6.27e-43
7	650	70.6	125	11	PCT-US93-1 Sequence 5, Applicatio	6.27e-43
8	647	70.2	125	11	PCT-US93-1 Sequence 31, Applicati	1.10e-42
9	641	69.6	123	7	US-08-478- Sequence 94, Applicat	5.89e-42
10	638	69.3	123	6	US-08-211- Sequence 141, Applicat	7.10e-42
11	637	69.2	123	6	US-08-211- Sequence 141, Applicat	7.10e-42
12	632	68.6	122	11	PCT-US93-0 Sequence 43, Applicati	1.80e-41
13	630	68.4	121	11	PCT-US93-0 Sequence 14, Applicati	2.52e-41
14	628	68.2	98	6	US-08-211- Sequence 118, Applicat	3.80e-41
15	628	68.2	122	11	PCT-US93-0 Sequence 12, Applicati	3.80e-41
16	627	68.1	125	7	US-07-942- Sequence 33, Applicati	4.88e-41
17	625	67.9	142	7	US-08-305- Sequence 2, Applicatio	5.55e-41
18	624	67.8	125	13	PCT-US95-0 Sequence 76, Applicati	8.02e-41
19	624	67.8	125	13	US-08-276- Sequence 76, Applicati	8.02e-41
20	621	67.4	125	13	PCT-US95-0 Sequence 72, Applicati	1.40e-40
21	621	67.4	125	7	US-08-276- Sequence 72, Applicati	1.40e-40
22	621	67.4	144	5	US-08-025- Sequence 2, Applicatio	1.40e-40

US-08-844-215-4.ra1

Thu Feb 26 07:06:00 1998

CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 543-9600
 CC TELEFAX: (415) 543-5043
 CC INFORMATION FOR SEQ ID NO: 46:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 119 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS:
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC FEATURE:
 CC NAME/KEY: Protein
 CC LOCATION: 1..119
 CC OTHER INFORMATION: /note= "Human fetal immunoglobulin
 CC OTHER INFORMATION: 56p1'CL Variable Heavy chain (V-H)"
 CC OTHER INFORMATION: 119 AA; 13279 MW; 79818 CN;
 CC SEQUENCE 119 AA; 13279 MW; 79818 CN;
 CC
 CC Query Match 72.68; Score 669; DB 7; Length 119;
 CC Best Local Similarity 75.28; Pred No 1.80e-44;
 CC Matches 94; Conservative 16; Mismatches 9; Indels 6; Gaps 4;
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 CC Db 115 VTSS 119
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 CC QY 121 VTSS 125
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 CC RESULT 2
 CC ID US-07-942-245-35 STANDARD: PRT; 120 AA.
 CC AC xxxxxx
 CC XX 01-JAN-1900
 CC DT
 CC DE Sequence 35, Application US/07942245.
 CC XX Sequence 35, Application US/07942245
 CC Patent No. 5639641
 CC GENERAL INFORMATION:
 CC APPLICANT: PEDERSEN, Jan T.
 CC APPLICANT: SEARLE, Stephen M.J.
 CC APPLICANT: REES, Anthony R.
 CC APPLICANT: POGUSKA, Michael A.
 CC APPLICANT: GUILD, Braydon C.
 CC TITLE OF INVENTION: SURFACE RESIDUE VENEERING OF RODENT
 CC TITLE OF INVENTION: ANTIBODIES
 CC NUMBER OF SEQUENCES: 522
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Sughrie, Mion, Zinn, Macpeak & Seas
 CC STREET: 2100 Pennsylvania Avenue, N.W.
 CC CITY: Washington
 CC STATE: D.C.
 CC COUNTRY: United States
 CC ZIP: 20037-3202
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPILER: HP 9000/700 Workstation
 CC OPERATING SYSTEM: UNIX
 CC SOFTWARE: In house
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/942,245
 CC FILING DATE: 09-SEP-1992
 CC CLASSIFICATION: 530
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (202) 293-7050
 CC TELEFAX: (202) 293-7860

CC TELEX: 6491103
 CC INFORMATION FOR SEQ ID NO: 35:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 120 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 120 AA; 13421 MW; 78517 CN;
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 CC Query Match 72.3%; Score 666; DB 7; Length 120;
 CC Best Local Similarity 74.2%; Pred. NO. 3.16e-44;
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 CC QY 121 VTSS 124
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 CC RESULT 3
 CC ID US-08-259-372A-2 STANDARD: PRT; 141 AA.
 CC AC xxxxxx
 CC XX 01-JAN-1900
 CC DT
 CC DE Sequence 2, Application US/08259372A.
 CC XX Sequence 2, Application US/08259372A
 CC Patent No. 5565354
 CC GENERAL INFORMATION:
 CC APPLICANT: Ostberg, Lars G.
 CC TITLE OF INVENTION: PRODUCTION OF HUMAN MONOCLONAL
 CC TITLE OF INVENTION: ANTIBODIES SPECIFIC FOR HEPATITIS B SURFACE ANTIG
 CC
 CC EN
 CC NUMBER OF SEQUENCES: 16
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend and Crew LLP
 CC STREET: Two Embarcadero Center, Eighth Floor
 CC CITY: San Francisco
 CC STATE: CA
 CC COUNTRY: USA
 CC ZIP: 94111-3834
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/259,372A
 CC FILING DATE: 14-JUN-1994
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/871,426
 CC FILING DATE: 21 APR-1992
 CC PRIOR APPLICATION DATA: US 07/676,036
 CC APPLICATION NUMBER: 27-MAR-1991
 CC FILING DATE: 27-MAR-1991
 CC PRIOR APPLICATION DATA: US 07/538,796
 CC APPLICATION NUMBER: 15-JUN-1990
 CC FILING DATE: 15-JUN-1990
 CC PRIOR APPLICATION DATA: US 07/192,754
 CC APPLICATION NUMBER: 11-MAY-1988
 CC FILING DATE: 11-MAY-1988
 CC PRIOR APPLICATION DATA: US 06/925,196
 CC APPLICATION NUMBER:

US-08-844-215-4-rai

Thu Feb 26 07:06:00 1998

CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.30
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/478,039
 CC FILING DATE: 07-JUN-1995
 CC CLASSIFICATION: 435
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 08/379,072
 CC FILING DATE: 25-JAN-1995
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/912,292
 CC FILING DATE: 10-JUL-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/856,281
 CC FILING DATE: 23-MAR-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/735,064
 CC FILING DATE: 25-JUL-1991
 CC NAME: Teskin Esq., Robin L.
 CC REGISTRATION NUMBER: 35,030
 CC REFERENCE/DOCKET NUMBER: 012712-160
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 703-836-6620
 CC TELEFAX: 703-836-2021
 CC INFORMATION FOR SEQ ID NO: 99:
 CC SEQUENCE CHARACTERISTICS:
 CC TYPE: amino acid
 CC LENGTH: 125 amino acids
 CC STRANDEDNESS: not relevant
 CC TOPOLOGY: not relevant
 CC MOLECULE TYPE: peptide
 CC POSITION IN GENOME:
 CC CHROMOSOME/SEGMENT: 18/2
 CC SEQUENCE 125 AA; 13543 MW; 93321 CN;
 Query Match 70.8%; Score 652; DB 7; Length 125;
 Best Local Similarity 69.8%; Pred. No. 4,32e-43;
 Matches 88; Conservative 18; Mismatches 18; Indels 2; Gaps 2;
 Db 1 EVQLVESGGGVQGRSLRSLCAASGFTFSYAMSVVRQAPGKGLWVAVXISGSGSTYY 60
 QY 1 EVQLVESGGGVQGRSLRSLCAASGFTFTYGMHVRQAPGKGLWVAVGISFDGSGNY 60
 Db 61 ADSVKGRFTISPDOSKNTLYLQMSLRADETAVYYCAKGOVLYG-SGSYHWFDPWGQT 119
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 Db 120 LVTVSS 125
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 RESULT 6 STANDARD: PRT: 125 AA.
 ID PCT-US93-10555-6
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 6, Application PC/TUS9310555.
 XX CC Sequence 6, Application PC/TUS9310555
 CC GENERAL INFORMATION:
 CC APPLICANT: SILVERMAN, GREGG J.
 CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
 CC THROUGH
 CC ATES TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
 CC TITLE OF INVENTION: THEREOF
 NUMBER OF SEQUENCES: 51
 CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jmbas & Imbitz
 CC STREET: 1880 Century Park East - Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/10555
 CC FILING DATE: 29-OCT-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Howells, Stacy L.
 CC REGISTRATION NUMBER: 34,842
 CC REFERENCE/DOCKET NUMBER: FO-2630
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 6:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 125 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
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 CC LOCATION: 1,125
 CC SEQUENCE 125 AA; 13612 MW; 90942 CN;
 Query Match 70.6%; Score 650; DB 11; Length 125;
 Best Local Similarity 68.8%; Pred. No. 6,27e-44;
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 Db 61 VDSVKGRFTISRDNKNTLYLQMSLRADETALYYCAKLTAAAGFTFTDYGMDWGQTLL 120
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 ID PCT-US93-10555-5
 XX AC xxxxxx
 XX DT 01-JAN-1900
 XX DE Sequence 5, Application PC/TUS9310555.
 XX CC Sequence 5, Application PC/TUS9310555
 CC GENERAL INFORMATION:
 CC APPLICANT: SILVERMAN, GREGG J.
 CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
 CC THROUGH
 CC ATES TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
 CC TITLE OF INVENTION: THEREOF

CC NUMBER OF SEQUENCES: 51
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Juba & Lubitz
 CC STREET: 1880 Century Park East - Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/10555
 CC FILING DATE: 29-OCT-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Howells, Stacy L.
 CC REGISTRATION NUMBER: 34,842
 CC REFERENCE/DOCKET NUMBER: PD-2630
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 5
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 125 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
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 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
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 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1..125
 CC SEQ SEQUENCE 125 AA; 13612 MW; 90692 CN;

Query Match 70.6%, Score 650, DE 11, Length 125;
 Best Local Similarity 68.8%, Pred No 6, 27e-43;
 Matches 86; Conservative 20; Mismatches 19, Indels 0, Gaps 0.

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 QY 61 ADSVKGFTIVSRNSRDTVFLQNSLPLEDTAVYYCATEGSPFGSIKGRYILENWSGQTL 120

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RESULT 8
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 DT 01-JAN-1900
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 CC GENERAL INFORMATION:
 CC APPLICANT: SILVERMAN, GREGG J.
 CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY PESTICID ANTI-BODIES
 CC THROUGH
 CC TITLE OF INVENTION: VACCINATION WITH A P-CELL SUPERNATANT AND CONJUG
 CC ATES
 CC TITLE OF INVENTION: THEREOF

CC NUMBER OF SEQUENCES: 51
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Juba & Lubitz
 CC STREET: 1880 Century Park East - Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/10555
 CC FILING DATE: 29-OCT-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Howells, Stacy L.
 CC REGISTRATION NUMBER: 34,842
 CC REFERENCE/DOCKET NUMBER: PD-2630
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 1
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 125 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: 18/2
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1..125
 CC SEQ SEQUENCE 125 AA; 13454 MW; 94507 CN;

Query Match 70.2%, Score 647, DE 11, Length 125;
 Best Local Similarity 69.8%, Pred No 1, 10e-42;
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 QY 1 EVQLVESGGGVQPGSSLRISCAASGFTTSTKTYGMHWVQAPKGLWVAVMSYSINRKY 60

Db 61 ADSVKGFTISPNKNTLYLQNSLPARTALYYCAKISTAASGFTTDTGMDCQTLL 119
 QY 61 ADSVKGFTIVSRNSRDTVFLQNSLPLEDTAVYYCATEGSPFGSIKGRYILENWSGQTL 119

Db 120 LTVSS 125
 QY 120 LTVSS 125

RESULT 9
 ID PCT-US93-07832-21 STANDARD PPT: 122 AA
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900
 XX
 DE Sequence 21, Application PCT/US93/07832.
 XX
 CC Sequence 21, Application PCT/US93/07832
 CC GENERAL INFORMATION:
 CC APPLICANT: Genentech, Inc.
 CC TITLE OF INVENTION: Immunoglobulin Variants
 CC NUMBER OF SEQUENCES: 40
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Genentech, Inc.
 CC STREET: 460 Point San Bruno Blvd
 CC CITY: South San Francisco

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CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22113-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/478,039
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/379,072
FILING DATE: 25-JAN-1995
APPLICATION DATA:
APPLICATION NUMBER: US 07/912,292
FILING DATE: 10-JUL-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/856,281
FILING DATE: 23-MAR-1992
APPLICATION DATA:
APPLICATION NUMBER: US 07/735,064
FILING DATE: 25-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Teskin Esq., Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/POCKET NUMBER: 012712-160
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 123 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
POSITION IN GENOME:
CHROMOSOME/SEGMENT: RF TS2
SEQUENCE 123 AA; 13515 MW; 82958 CN;
Query Match 69.3%; Score 638; DB 7; Length 123;
Best Local Similarity 69.1%; Pred. No. 5,89e-42;
Matches 85; Conservative 20; Mismatches 17; Indels 1; Gaps 1;
1 QVQLVESGGVGVPGQRSLRLSCAASGFTFSYGMHWVROAPGKGLWVYVSYDGSNEYF 60
1 EVQLLESGGVGVPGQRSLRLSCAASGFTFTYGMHWVROAPGKGLWVAGISFDGSNYY 60
61 ADSVKGRFTISRDNSNTLYGMNSLRLEDATVYVCARDVAVYASVFFIDSPDIWGQGT 120
61 ADSVKGRFIVSRDNRSDTVFIOMSLRLEDATVYVCATE-GSPFGS1KGRVYLENW3QGT 119
121 GVT 123
122 LVT 122
RESULT 11
ID US-08-211-202-141 STANDARD: PRT: 116 AA.
XX XXXXXX
XX AC
DT 01-JAN-1900
DE Sequence 141, Application US/08211202.
Sequence 141, Application US/08211202
Patent No. 5565332
GENERAL INFORMATION:
APPLICANT: HOOGEBOOM, Hendricus Renerus Jacobus Matieus

```

CC APPLICANT: BAIER, Michael
CC APPLICANT: JESPER, Laurent Stephane Anne Therese
CC APPLICANT: WINTER, Gregory Paul
CC TITLE OF INVENTION: Production of chimeric antibodies - a
CC TITLE OF INVENTION: combinatorial approach
CC NUMBER OF SEQUENCES: 144
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
CC ADDRESSEE: Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: USA
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1 0, Version #1 25 (EPO)
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/211,202
CC FILING DATE: 23-SEP-1992
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GR 9120252.3
CC FILING DATE: 23-SEP-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GR 9120377.8
CC FILING DATE: 25-SEP-1991
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GR 9206318.9
CC FILING DATE: 24-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: GR 9206372.5
CC FILING DATE: 24-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: PCT/FR92/00883
CC FILING DATE: 15-MAY-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: David W. Clough
CC REGISTRATION NUMBER: 36 107
CC REFERENCE/DOCKET NUMBER: 28111/31950
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312-474-6300
CC TELEFAX: 312-474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 141:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 116 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 116 AA: 12678 MW; 72426 CN;
SQ
Query Match 69.2%; Score 637; DB 6; Length 116;
Best Local Similarity 73.7%; Pred. No. 7.10e-42;
Matches 87; Conservative 16; Mismatches 13; Indels 2; Gaps 2;
Db 1 QVQLVESGGVVQPGSPSLPSCAASGFTFESSYAMHWVPQAPGKGLWVAIVSYDGSNKYY 60
QY 1 EVQLLESGGIVGQPGSPSLPSCAASGFTFKTYGMHWVPQAPGKGLWVAIVSYDGSNQYY 60
Db 61 ADSVKGRFTISPEKNTLYLQMSLSRAKLTAVYYCAS-GP-VCSGGSGSPFFVWJG 116
QY 61 ADSVKGRFTVSRDNPQIVFLQMSLPLEDTAVYYCATGSPFGSIKGPYYLENWGGG 118
RESULT 12
ID PCT-US93-08435-43 STANDARD: PRT: 122 AA.
XX
AC xxxxxx
XX 01-JAN-1900
DT

XX Sequence 43, Application PC/TUS9308435.
DE
XX Sequence 43, Application PC/TUS9308435.
XX GENERAL INFORMATION:
CC APPLICANT: SmithKline Beecham, Corporation
CC APPLICANT: U.S. Government, Secretary of
CC APPLICANT: the Navy
CC APPLICANT: U.S. Government, Secretary of
CC APPLICANT: the Army
CC TITLE OF INVENTION: Novel Antibodies for Confering Passive
CC TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
CC NUMBER OF SEQUENCES: 61
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Howson and Howson
CC STREET: Box 457, 321 Norristown Road
CC CITY: Spring House
CC STATE: PA
CC COUNTRY: USA
CC ZIP: 19477
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/08435
CC FILING DATE:
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/941,654
CC FILING DATE: 09-SEP-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Bak, Mary E.
CC REGISTRATION NUMBER: 31,215
CC REFERENCE/DOCKET NUMBER: SPC P50107
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (215) 540-9200
CC TELEFAX: (215) 540-5818
CC INFORMATION FOR SEQ ID NO: 43:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 122 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 122 AA: 13313 MW; 87403 CN;
SQ
Query Match 68.5%; Score 632; DB 11; Length 122;
Best Local Similarity 71.2%; Pred. No. 1.80e-41;
Matches 89; Conservative 15; Mismatches 18; Indels 3; Gaps 3;
Db 1 EVQLLESGGIVGQPGSPSLPSCAASGFTFESSYAMHWVPQAPGKGLWVAIVSYDGSYIYY 60
QY 1 EVQLLESGGIVGQPGSPSLPSCAASGFTFKTYGMHWVPQAPGKGLWVAIVSYDGSNQYY 60
Db 61 PQTIVTGFTTISEKSNKNTLYLQMSLSRAEDTAVYYCASLIY-VG-YDG-YAMCYWJGJIL 117
QY 61 ADSVKGRFTVSRDNPQIVFLQMSLPLEDTAVYYCATGSPFGSIKGPYYLENWJGJIL 120
Db 118 VTSS 122
QY 121 VTSS 125
RESULT 13
ID PCT-US93-08435-14 STANDARD: PRT: 122 AA.
XX
AC xxxxxx
XX 01-JAN-1900
DT Sequence 14, Application PC/TUS9308435.
XX

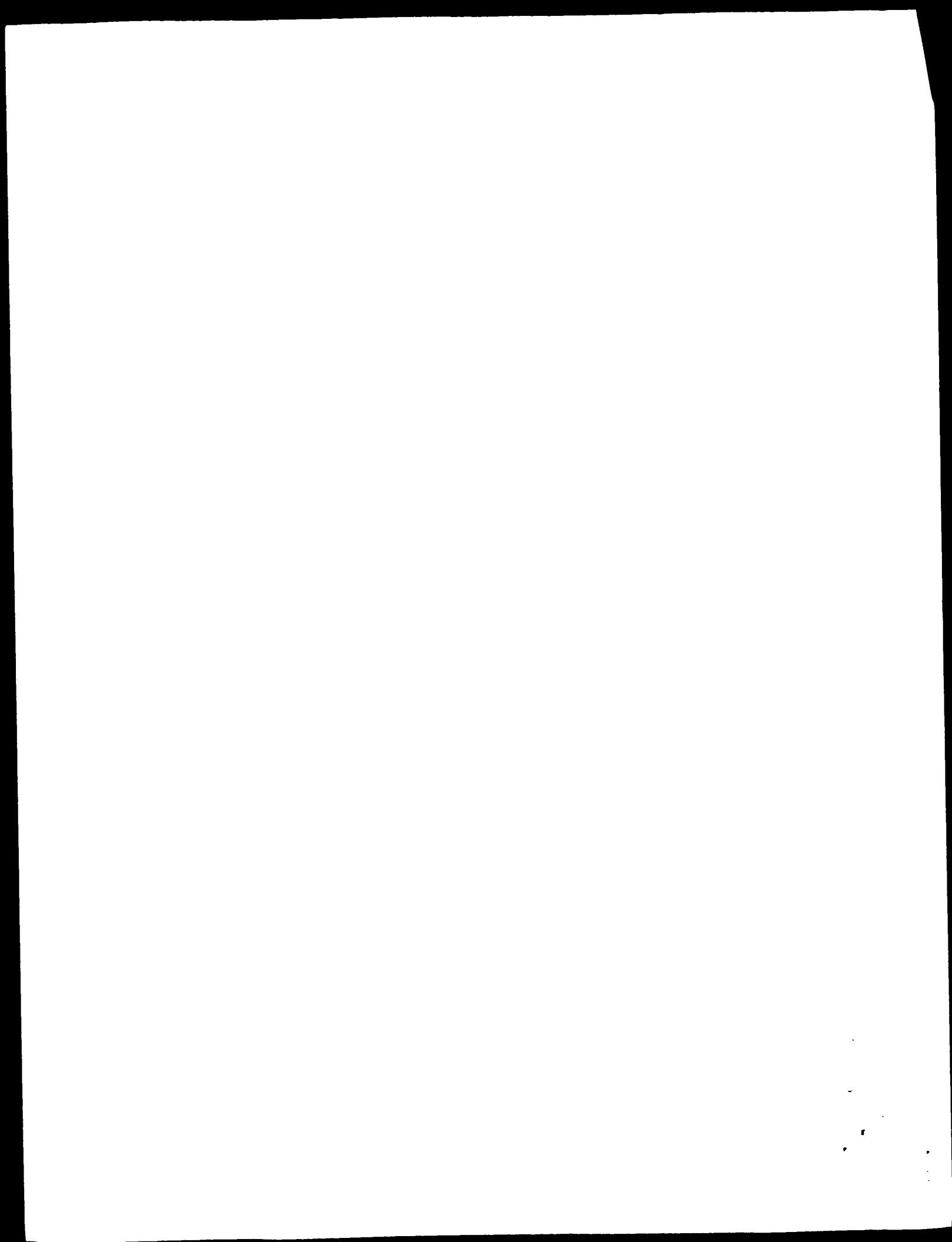
US-08-844-215-4-rai

Thu Feb 26 07:06:00 1998

Sequence 14. Application PC/TUS9308435
 GENERAL INFORMATION:
 APPLICANT: SmithKline Beecham, Corporation
 APPLICANT: U. S. Government, Secretary of
 APPLICANT: the Navy
 APPLICANT: U. S. Government, Secretary of
 APPLICANT: the Army
 TITLE OF INVENTION: Novel Antibodies for Conferring Passive
 TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howson and Howson
 STREET: Box 457, 321 Norristown Road
 CITY: Spring House
 STATE: PA
 COUNTRY: USA
 ZIP: 19477
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/08435
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/941,654
 FILING DATE: 09-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Bak, Mary E.
 REGISTRATION NUMBER: 31,215
 REFERENCE/DOCKET NUMBER: SBC P50107
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 540-5818
 TELEFAX: (215) 540-9200
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 122 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE 122 AA: 13329 MW; 88138 CN;
 Query Match 68.4%; Score 630; DB 11; Length 122;
 Best Local Similarity 70.4%; Pred. No. 2.62e-41;
 Matches 88; Conservative 16; Mismatches 18; Indels 3; Gaps 3;
 Db 1 EVOLVESGGVGVQPGSLRLSCAASGFTFSYAMSVYRQAPGKLEWVSEISDGGSYTY 60
 QY 1 EVOLVESGGVGVQPGSLRLSCAASGFTFKYGMHVRQAPGKLEWVAGISFDGSGNOYY 60
 Db 61 PTVTVGRTTISRDNSKNTLYQMNSLRLEDYAVYGCASLIY-YG-YDG-YAMDYWGOGTL 117
 QY 61 ADSVKGRFTIVSPDNRDTVFLQMSLRLEDYAVYGCASLIY-YG-YDG-YAMDYWGOGTL 120
 Db 118 VTVSS 122
 QY 121 VTVSS 125
 RESULT 14
 ID US-08-211-202-118 STANDARD: PPT: 98 AA.
 XX
 AC xxxxxx
 XX
 DT 01-JAN-1900
 XX
 DE Sequence 118, Application US/08211202.
 XX
 DE Sequence 118, Application US/08211202
 CC Patent No. 5565332
 CC
 CC GENERAL INFORMATION:
 APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Mattheus
 APPLICANT: BAIER, Michael
 APPLICANT: JESPEERS, Laurey Stephane Anne Therese
 APPLICANT: WINTER, Gregory Paul
 TITLE OF INVENTION: Production of chimeric antibodies - a
 TITLE OF INVENTION: combinatorial approach
 NUMBER OF SEQUENCES: 144
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
 ADDRESSEE: Borun
 STREET: 6300 Sears Tower, 233 South Wacker Drive
 CITY: Chicago
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60606-6402
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/211,202
 FILING DATE: 23-SEP-1992
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9120252.3
 FILING DATE: 23-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9120377.8
 FILING DATE: 25-SEP-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206318.9
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9206372.6
 FILING DATE: 24-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/GB92/00883
 FILING DATE: 15-MAY-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: David W. Clough
 REGISTRATION NUMBER: 36,107
 REFERENCE/DOCKET NUMBER: 28111/31960
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312-474-6300
 TELEFAX: 312-474-0448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 118:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 98 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE 98 AA: 10838 MW; 50043 CN;
 Query Match 68.2%; Score 628; DB 6; Length 98;
 Best Local Similarity 83.5%; Pred. No. 3.80e-41;
 Matches 81; Conservative 11; Mismatches 5; Indels 0; Gaps 0;
 Db 1 QVQLVESGGGVQPGSLRLSCAASGFTFSYAMHVRQAPGKLEWAVISYDGSNKYY 60
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 Db 61 ADSVKGRFTISRDNSKNTLYQMNSLRLEDYAVYCA 97
 QY 61 ADSVKGRFTIVSPDNRDTVFLQMSLRLEDYAVYCA 97
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 ID PCT-US93/08435-12 STANDARD: PPT: 122 AA.
 XX
 AC xxxxxx
 XX

DT 01-JAN-1909
 XX
 DE Sequence 12, Application PC/TUS9308435.
 XX
 CC Sequence 12, Application PC/TUS9308435
 CC GENERAL INFORMATION:
 CC APPLICANT: SmithKline Beecham, Corporation
 CC APPLICANT: U. S. Government, Secretary of
 CC APPLICANT: the Navy
 CC APPLICANT: U. S. Government, Secretary of
 CC APPLICANT: the Army
 CC TITLE OF INVENTION: Novel Antibodies for Conferring Passive
 CC TITLE OF INVENTION: Immunity Against Infection by a Pathogen in Man
 CC NUMBER OF SEQUENCES: 61
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Howson and Howson
 CC STREET: Box 457, 321 Norristown Road
 CC CITY: Spring House
 CC STATE: PA
 CC COUNTRY: USA
 CC ZIP: 19477
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/08435
 CC FILING DATE:
 CC CLASSIFICATION:
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/941,654
 CC FILING DATE: 09-SEP-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Bak, Mary E.
 CC REGISTRATION NUMBER: 31,215
 CC REFERENCE/DOCKET NUMBER: SRC P50107
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (215) 540-9200
 CC TELEFAX: (215) 540-5818
 CC INFORMATION FOR SEQ ID NO: 12:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 122 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 122 AA; 13370 MW; 87746 CN;
 SQ
 Query Match 68.2%; Score 628; DB 11; Length 122;
 Best Local Similarity 70.4%; Pred. No. 3.80e-41;
 Matches 88; Conservative 15; Mismatches 19; Indels 3; Caps 3;
 Db 1 EVOLLESGGLVOPGSLPLSCAASGTFESSYAMSWVRQAPGKLEWVSEISDGGSYTY 60
 QY 1 EVOLLESGGVVQPSRLSCAASGFTFKTYGMHWVRQAPGKLEWVAGISFDGSNQYY 60
 Db 61 PDVTIGRTISPDNSKNTLYLQMSLRAEDTAVYYCAKLIY-YG-YDG-YAMDYWGQGL 117
 QY 61 ADSVKGRFTVSPDNRDIVFLQMSLPLEDTAVYYCATEGSPFGSIKGPYYLENWGQGL 120
 Db 118 VTVSS 122
 QY 121 VTVSS 125

Search completed: Tue Feb 24 07:37:23 1998
 Job time : 12 secs.



M I S E R E

(TM)

Release 2.1D John F. Collins, Biocomputing Research Unit
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Distribution rights by Intelligentics, Inc.
MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:10:11 1998; Waspar time 7.49 Seconds
231.859 Million cell updates/sec
Tabular output not generated.
Title: >US-08-844-215-4
Description: (1-125) from US0884215.pep
Perfect Score: 921
Sequence: 1 EVOLLESGGVGVGPGRSLRL... IKGPYYLENWGGTLTVSS 125

Scoring table: PAM 150
Gap 11
Searched: 111726 seqs, 13889129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: a-geneseq30
1 part: 2 part2 3 part3 4 part4 5 part5 6 part6 7 part7
8 part8 9 part9 10 part10 11 part11 12 part12 13 part13
14 part14 15 part15 16 part16 17 part17 18 part18
19 part19 20 part20 21 part21 22 part22 23 part23
Statistics: Mean 30.277; Variance 155.246; scale 0.195

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES					Pred. No.	
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1	690	74.9	192	7	R38161	Sequence of the heavy
2	681	73.9	193	23	W15331	Anti-melanoma antibody
3	680	73.8	506	2	W12134	OPF 3 of 489 human MA
4	677	73.5	123	23	W15334	Anti-TGF beta-1 scfv
5	674	73.2	141	13	W15333	Anti-interleukin-1-a1
6	669	72.6	119	19	R95216	Human foetal immunogl
7	668	72.5	123	23	W15335	Anti-TGF beta-1 scfv
8	666	72.3	115	4	P23571	Heavy chain VH3 scfv
9	665	72.3	120	17	P52064	Heavy chain variable
10	657	71.3	141	19	W01522	Monoclonal antibody f
11	657	71.3	141	23	W24984	Monoclonal antibody p
12	653	70.9	140	23	W13524	Anti-melanoma antibody
13	651	70.7	143	9	P54047	Sequence of the VH re
14	650	70.6	156	9	P54788	SpA-reactive IgM heav
15	650	70.6	156	9	P54789	SpA-reactive IgM heav
16	649	70.5	123	22	W15335	Anti-TGF beta-1 scfv
17	639	69.4	111	2	P12275	Anti-human Pdp HAM-R
18	638	69.3	124	23	W15337	Anti-melanoma antibody
19	638	69.3	125	9	P54784	SpA-reactive IgM heav
20	638	69.3	140	14	P84480	Anti-human IL-4 human

21	638	69.3	467	14	R80617	Anti-human IL-4 human
22	630	69.1	120	5	P23746	Heavy chain variable
23	624	69.8	117	12	R65321	Human immunoglobulin
24	623	69.7	142	6	R21534	M4H7 MAB heavy chain
25	632	69.6	122	9	P50315	Humanized heavy chain
26	631	69.5	126	7	R38163	KOL heavy chain
27	630	69.4	122	9	P50312	Humanized heavy chain
28	629	69.3	124	23	W15333	Anti-melanoma antibody
29	629	69.3	459	8	R42056	Human anti-HBs heavy
30	628	69.2	112	2	P12274	Anti-human Pdp PEG-A
31	628	69.2	117	23	W15523	Anti-TGF beta-2 scfv
32	628	69.2	122	9	P50311	Humanized heavy chain
33	627	69.1	121	3	R13183	Variable region of u
34	627	69.1	221	10	P56234	162-109/112-61/h1-125
35	626	69.0	115	23	W15522	Anti-TGF beta-3 scfv
36	625	69.0	123	22	W08582	Human antibody C4.1 h
37	625	67.9	142	23	W2251	64-863 antibody H586
38	624	67.8	122	6	R30773	Consensus humanised m
39	624	67.8	125	10	R54208	Anti-HIV gp120 immuno
40	624	67.8	125	19	W01255	VH region of HIV neut
41	623	67.6	140	8	R41469	MAB 25D2 humanised be
42	622	67.5	116	9	P34285	Human TNP binding ant
43	621	67.4	125	19	W01251	VH region of HIV neut
44	621	67.4	125	10	R54248	Anti-HIV gp120 immuno
45	619	67.2	125	4	P23745	Recombinant heavy cha

ALIGNMENTS

RESULT 1
ID R38161 standard; Protein: 192 AA.
AC R38161:
DI 01-OCT-1993 (first entry)
DE Sequence of the heavy chain variable region (VH) of human
DE immunoglobulin G3 (1963) produced by transformed human B-cell line
DE 88BV59, ATCC CRL 10624.
KW B-cell; immunoglobulin g; cancer; tumour.
OS Homo sapiens.
PH Key Location/Qualifiers
FT Region 1..113
FT /label=VAR
FT /note="1st AA is denoted AA#1"
FT Region 31..49
FT /label= CDR 1
FT Region 50..94
FT /label= CDR 2
FT Region 95..111
FT /label= CDR 3
FT Region 112..223
FT /label= CH 1
FT Region 224..238
FT /label= Hinge
FT Region 239..242
FT /label= Fab'
PN FP-546634-A
PD 16-JUN-1993.
PF 09-DEC-1992; 203827.
PF 13-DEC-1991; US-807300.
PA (ALKU) AKZO NV
PI Crichton VZ; Haspel MV, Kobrin BJ;
DP WFI 93-196019/24.
DE N-TSDE; Q43772.
FT transformed human B-cell line for monoclonal antibody prodn. for
FT cancer diagnosis - prepd from peripheral blood B-cells of cancer
FT patients actively immunised with autologous tumour antigen, for
FT treating cancers
PS Claim 5, Fig 2, 18pp, English.
CC Q43772 encodes the complete heavy chain from the leader through AAs
CC 242. 88BV59 uses VHIII and a D region which may have resulted from
CC intra-D-D recombination and/or gene conversion along with somatic
CC mutation. It is radically different from any germ line D region. It
CC utilises germ line JH3 it is of note that a cysteine at AA posn 50
CC (AA No. 78 in R38161) is present within the 88BV59 VH. No other

KW post myocardial infarction; post-angioplasty restenosis;
 KW scleroderma; vascular disease; cataract; glaucoma; scarring;
 KW glomerulonephritis; osteoporosis; immune disease; inflammation;
 KW rheumatoid arthritis; macrophage deficiency disease;
 KW macrophage pathogen infection; therapy.
 OS Homo sapiens.
 PN GB2305921-A
 PD 23-APP-1997
 PF 07-OCT-1996; 020920
 PR 19-JAN-1996; GB-001081.
 PR 06-OCT-1995; GB-020486.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PI Bacon L, Green JA, Jackson PH, Johnson KS, Pope AP,
 PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ.
 PI Wilton AJ.
 DR WPI: 97-215360/20.
 DR N-PSDB: T60380.
 PT Agent contg. antigen-binding domain of human antibody to
 PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
 PT it, used to neutralise effects of TGF- α for control of fibrosis,
 PT immune and inflammatory disease
 PT Claim 16, Fig 1a(1), 18app. English.
 PS This polypeptide sequence comprises the VH domain of human scFv
 CC antibody 1B2 (also known as 7A3), which is specific for
 CC transforming growth factor (TGF) beta-1. It is encoded by a gene
 CC (T60380) isolated from a peripheral blood lymphocyte library. The
 CC antigen-binding domains of human antibodies (see W15522-40) to TGF
 CC beta-1 and/or beta-2 can be used to counter the adverse effects of
 CC TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or
 CC keloid scarring, lung fibrosis, arterial injury, proliferative
 CC retinopathy, retinal detachment, adult respiratory distress syndrome,
 CC liver cirrhosis, post myocardial infarction, post-angioplasty
 CC restenosis, scleroderma, vascular disorders, cataract, glaucoma, or
 CC esp. neural scarring and glomerulonephritis, also (not claimed)
 CC osteoporosis), or (ii) immune and inflammatory diseases (rheumatoid
 CC arthritis, macrophage deficiency diseases or macrophage pathogen
 CC infection). Nucleic acids encoding human antibody VH and VL can be
 CC used for prodn. of recombinant antigen-binding domains. These are
 CC highly specific, have low dissociation constants (K_d less than 5
 CC nM) and low IC50s for neutralisation.
 CC Sequence 123 AA.

Query Match 73.5%; Score 677; DB 23; Length 123;
 Best Local Similarity 73.6%; Pred. NG: 1.30e-44;
 Matches 92; Conservative 16; Mismatches 15; Indels 2; Gaps 2;
 Db 1 qvqlvesggvqprsrllscasagffssygmhvwraqpckglewrvavisdgskyy 60
 QY 1 EVOLLESGGGVQPGSPSLSCAASFTFTYGMHWVQAPCKGLEWVAGISFDGSGNYY 60
 Db 61 adsvkarftisrdnsknltlqmslraedtavvycaqtge-yssydsdg-vdvwgkatt 118
 QY 61 AUSVKGFVSPNSPDTVFLQWSSLPLEDTAVVYVATGSPSPGSKPKPYVLENWGGTTL 120
 Db 119 vtvs 123
 QY 121 VTVSS 125

RESULT 5

ID R75393 standard; Protein: 141 AA.
 AC R75393;
 DT 04-NOV-1995 (first entry)
 DE Anti-interleukin-1-alpha human monoclonal antibody VH segment.
 KW Monoclonal antibody; interleukin-1-alpha; cytokine;
 KW antiinflammatory; prophylactic; therapeutic.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "signal peptide"
 FT Region 20..49
 FT /note= "Framework (FP) 1 (-1 to -30)"
 FT /note= 50..54

FT /note= "CDR 1 (+31 to +35)"
 FT Region 55..68
 FT /note= "FR 2 (+36 to +49)"
 FT Region 64..85
 FT /note= "CDR 2 (+50 to +66)"
 FT Region 86..117
 FT /note= "FR 3 (+67 to +98)"
 FT Region 118..129
 FT /note= "CDR 3 (+99 to +110)"
 FT Region 130..141
 FT /note= "JH 1 (-111 to -122)"
 PN WO9514780-A.
 PD 01-JUN-1995.
 PF 21-NOV-1994; 013188
 PR 23-NOV-1993; EP-402846.
 PA (SCHE) SCHERING-PLOUGH.
 PI Bancheureau J, Djossou O, Fossiez F, Garonne P;
 DR WPI: 95-206937/27.
 DR N-PSDB: Q87236
 PT Human monoclonal antibody against a human cytokine - used to mfr a
 PT medicament to treat inflammation.
 PS Claim 7; Page 44-45; 70pp; English.
 CC The sequence represents the variable heavy chain segment of a human
 CC monoclonal antibody (HuMab) against interleukin-1-alpha. The Mab is
 CC of subclass IgG4 and binds to lymphokines/monokines with an affinity
 CC of 10(9)/M. The Mab or fragment (Fv, single-chain Fv, Fab or F(ab')
 CC 2) is used in the treatment of inflammation e.g. rheumatoid
 CC arthritis, osteoarthritis and inflammatory bowel diseases, and in
 CC the treatment of psoriasis, allergic shock, graft vs host
 CC disease and tumours. The Mab or fragment can also be used for
 CC diagnosis.
 CC Sequence 141 AA;

Query Match 73.2%; Score 674; DB 13; Length 141;
 Best Local Similarity 73.6%; Pred. No. 2.29e-44;
 Matches 92; Conservative 15; Mismatches 15; Indels 3; Gaps 2;

Db 20 qvqlvesggvqprsrllscasagffssygmhvwraqpckglewrvavisdgskyy 79
 QY 1 EVOLLESGGGVQPGSPSLSCAASFTFTYGMHWVQAPCKGLEWVAGISFDGSGNYY 60
 Db 80 aevskarfisrdnsknltlqmslraedtavvycaqtge-yssydsdg-vdvwgkatt 126
 QY 61 AUSVKGFVSPNSPDTVFLQWSSLPLEDTAVVYVATGSPSPGSKPKPYVLENWGGTTL 120
 Db 137 vtfs 141
 QY 121 VTVSS 125

RESULT 6

ID R95216 standard; protein: 112 AA.
 AC R95216;
 DT 16-DEC-1996 (first entry)
 DE Human foetal immunoglobulin 56p1/01 variable heavy chain.
 KW Antibody; fusion protein; single chain; inhibition; tumour;
 KW diagnosis; detection; imaging; immunotoxin; targeting; assay;
 KW immunoassay; Lewis(Y) carbohydrate antigen.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Domain 31..35
 FT /label= CDR 1.
 FT Domain 50..66
 FT /label= CDR 2.
 FT Domain 99..108
 FT /label= CDR 3.
 PN WO9613594-A1.
 PD 09-MAY-1996.
 PF 26-OCT-1995; 013811.
 PR 28-OCT-1994; US-331398.
 PR 28-OCT-1994; US-331396.
 PR 28-OCT-1994; US-331397.

Claim 16; Fig 1a(ii): 184pp; English.
This polypeptide comprises the VH domain of human scFv antibody 31C9, which is specific for transforming growth factor (TGF) beta-1. It is encoded by a gene (T60381) isolated from a large single chain Fv library. The antigen-binding domains of human antibodies (see W5522-40) to TGF beta-1 and/or beta-2 can be used to counter the adverse effects of TGF beta, such as (i) promotion of fibrosis (in dermal, ocular or keloid scarring, lung fibrosis, arterial injury, proliferative retinopathy, retinal detachment, adult respiratory distress syndrome, liver cirrhosis, post myocardial infarction, post-angioplasty restenosis, scleroderma, vascular disorders, cataract, glaucoma, or esp. neural scarring and glomerulonephritis), also (not claimed) osteoporosis), or (ii) immune and inflammatory diseases (e.g. rheumatoid arthritis, macrophage deficiency diseases or macrophage pathocen infection). Nucleic acids encoding human antibody VH and VL can be used for prodn. of recombinant antigen-binding domains. These are highly specific, have low dissociation constants (pref. less than 5 nM) and low IC50s for neutralisation.

Query Match 72.5%; Score 668; DB 23; Length 123;
Best Local Similarity 73.5%; Pred. No. 7.07e-44;
Matches 92; Conservative 15; Mismatches 16; Indels 2; Gaps 2;

1 qvqlvsgggvqpgqsrllscasgftfssygmhvwrrqpdkalewvavisydskyy 60
1 EVQLLESGGSGVVGFGSKRLSCAASGFTFKYCKMHVWVQAPGKGLPWWAGISPTKSNQYY 60
61 adsvkgrftisrdnsntlylqmslraedtavvyccarr-s---a-rt-yfydwygggtl 114
61 ADSVKGFRIVSRDNRDTVFLQMSLRLEDTAVYYCATEGSPFGSIKGRYYLLENNWGQGTLL 120
119 vtvs 123
121 VTSS 125

RESULT 8
ID R22571 standard; Protein: 115 AA.
AC R22571;
DE 21-MAY-1992 (first entry)
DE Heavy chain VH3.5 from BSA binding scFv fragment.
KW Fd; bacteriophage; gene III; filamentous; phagemid; capsid; coat;
KW pilus; gsp; binding; adsorption; gene VIII; diverse repertoire;
KW specific binding pairs; replicable genetic display package; human.
OS Homo sapiens.
PN WO9201047-A.
PD 23-JAN-1992.
PF 10-JUL-1991; G01134.
PR 10-JUL-1990; GB-015198.
PR 19-OCT-1990; GB-022845.
PR 12-NOV-1990; GB-024503.
PR 06-MAR-1991; GB-004744.
PR 15-MAY-1991; GB-010549.
PA (CMB-) CAMBRIDGE ANTIBODY.
PA (MED-) MED RES COUNCIL.
PI McCafferty J, Pope AR, Johnson KS, Hoogenboom HKJ, Griffiths AD;
PI Jackson RH, Holliger KP, Marks JD, Clackson TP, Chiswell DJ;
PI Winter GP, Bonnett TP;
PI WPI: 92-056862/07.
DR Producing members of specific binding pairs - by expression in
PT recombinant host cells with a secreted replicable genetic
PT display package.
PS Table 11; Page 152; 109pp; English.
CC PCP was used to prepare a human scFv library from RNA from white
CC blood cells from an unimmunised donor. Heavy chains from IgG and
CC IgM antibodies were amplified separately. Four separate libraries
CC were generated (IgG-K, IgG-lambda, IgM-K and IgM-lambda). The
CC purified scFv fragments were ligated into the phagemid pHE1 for
CC expression on the surface of fd bacteriophage as gene III fusions.
CC The clones were then subjected to affinity selection for binding
CC to phox:BSA by selection on tubes followed by analysis by ELISA. Of

(USSH) US DEPT HEALTH & HUMAN SERVICES.
PA Benhar I, Brinkmann U, Fitzgerald D, Jung S, Lee R;
PI Padlan EA, Pai L, Pastan I, Willingham W;
DR WPI: 96-251462/25.
PT Single chain fusion proteins and antibodies - useful to diagnose and
PT treat cancer, specifically bind Lewis(X) related carbohydrate
PT antigen
PS Example 13; Figure 11A; 116pp; English.
CC A novel recombinant DNA molecule which encodes a single chain fusion
CC protein or antibody comprising the Fv region of both the light and
CC heavy chains of an antibody (Ab) fused together, and an effector
CC molecule, where the fusion protein or Ab has the binding specificity
CC of monoclonal Ab (Mab) B1, B3 or B5, can be used for the production
CC of such fusion proteins or antibodies. The fusion proteins can be
CC used in compositions as an immunotoxin to inhibit tumour cell growth
CC The single chain antibody can be used to detect the presence of
CC absence of cells bearing a Lewis(X) carbohydrate antigen in a
CC patient. The antibodies are also useful as multiple targeting
CC moieties, providing at least 2 kinds of biological activity. They
CC can also be used in diagnostic assays and for the imaging of tumours
CC when attached to a radiolabel and for the pathological diagnosis of
CC tumours. Humanised antibodies are less immunogenic than the mouse
CC Mabs B1, B3 and B5, making them more suitable for long term
CC treatment.
CC Sequence 119 AA;

Query Match 73.5%; Score 669; DB 18; Length 119;
Best Local Similarity 75.2%; Pred. No. 5.86e-44;
Matches 94; Conservative 16; Mismatches 9; Indels 6; Gaps 4;

1 qvelvsgggvqpgqsrllscasgftfssygmhvwrrqpdkalewvavisydskyy 60
1 EVQLLESGGSGVVGFGSKRLSCAASGFTFKYCKMHVWVQAPGKGLPWWAGISPTKSNQYY 60
61 adsvkgrftisrdnsntlylqmslraedtavvyccarr-s---a-rt-yfydwygggtl 114
61 ADSVKGFRIVSRDNRDTVFLQMSLRLEDTAVYYCATEGSPFGSIKGRYYLLENNWGQGTLL 120
115 vtvs 119
121 VTSS 125

RESULT 7
ID W15535 standard; Protein: 123 AA.
AC W15535;
DE 27-NOV-1997 (first entry)
DE Anti-TGF beta-1 scFv antibody 31C9 VH domain.
DE Transforming growth factor beta-1; TGF-beta-1; human;
KW antibody engineering; scFv; phage display; lung fibrosis;
KW arterial injury; proliferative retinopathy; retinal detachment;
KW adult respiratory distress syndrome; liver cirrhosis;
KW post myocardial infarction; post-angioplasty restenosis;
KW scleroderma; vascular disease; cataract; glaucoma; scarring;
KW glomerulonephritis; osteoporosis; immune disease; inflammation;
KW rheumatoid arthritis; macrophage deficiency disease;
KW macrophage pathocen infection; therapy.
OS Homo sapiens.
PN GB2305921-A.
PD 23-APR-1997.
PF 07-OCT-1996; 020920.
PR 19-JAN-1996; GB-001081.
PR 06-OCT-1995; GB-020486.
PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
PI Wilton AJ;
PI WPI: 97-215360/20.
DR N-P5DB; T60381.
PT Agent contg. antigen-binding domain of human antibody to
PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT immune and inflammatory disease

US-08-844-215-4.rag

Thu Feb 26 07:05:59 1998

PD 11-MAY-1994.
 PF 29-OCT-1993: U10555.
 PR 30-OCT-1992: US-969936.
 PA (REGC) UNIV CALIFORNIA.
 PI Silverman GJ:
 DR WPI. 94-167127/20.
 PT Stimulating prode. of variable region gene family restricted
 PT antibodies - through B-cell super-antigen vaccination
 PS Disclosure; Page 71: 130pp; English.
 CC A B-cell superantigen (sAg) is a fragment of SpA D domain that
 CC specifically binds the Fab portion of variable region restricted
 CC antibodies. The sAg is used to enhance production of VH, especially
 CC VH3, restricted Abs. During attempts to identify sAgs, aa sequences
 CC (R54784-801) of H chains from Ig reactive with mod-SpA, and aa and
 CC DNA sequences (R54802-16, Q64842-56) of VH regions of SpA binders
 CC obtained from combinatorial libraries were determined. IgM protein
 CC RIV is derived from the germline configuration of a VH gene
 CC segment.
 SQ Sequence 125 AA;

Query Match 70.6%; Score 650; DB 9; Length 125;
 Best Local Similarity 68.8%; Pred. No. 2,07e-42;
 Matches 86; Conservative 20; Mismatches 19; Indels 0; Gaps 0;

Db 1 evqlvesgggvgvqgsrlrlscaasgftsfssfamhvrqapkglewavmsysgdnkyy 60
 QY 1 EVQLLESGGGVWQPGRSLRLSCLCAASGFTFTKTYGMHWVRQAPKGLEWVAGISFDGSGNQYY 60
 Db 61 vdsvkgrftisrdnskntlylqmnslraedtalycaklstaasgftfdtygmdwgqttl 120
 QY 61 ADSVKGRFIVSRDNRSDTVFLQWSSLELEDIAVYYCATEGSPFGSIKGRYYLENWGQGTLL 120
 Db 121 vtvs 125
 QY 121 VTVSS 125

Search completed: Tue Feb 24 07:10:46 1998
 Job time : 35 secs.

Thu Feb 26 07:05:58 1998

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AC P01743; 1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (HG3).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83144028.
RA RECHAVI G., RAM D., GLAZER L., ZAKUT P., GIVOL D.:
RL PROC. NATL. ACAD. SCI. U.S.A. 80:855-859(1983).
DR EMBL; J00240; G553411.
DR PIR; A02024; HVH0HG.
DR HSP; P01810; LFVB.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT CHAIN 1 19 IG HEAVY CHAIN V REGION (HG3).
FT NON_TER 20 117
FT SEQUENCE 117 AA; 12946 MW; BCC8B1DB CRC32;
SQ
Query Match 52.9%; Score 484; DB 5; Length 117;
Best Local Similarity 70.7%; Pred. No. 4.63e-88;
Matches 70; Conservative 15; Mismatches 13; Indels 1; Gaps 1;
Db 20 qvqlv-qsgaevkpgasvkskasytftqymhvwirgagpggglewmglnpsggsts 78
QY 1 EVOLLEQSGAEVKKPGSSVKVSKASGGTFSGHVSWVRQAPGQGLEWMGGSISFFGTSN 60
Db 79 yaqkfgrvtrtdstsvymelsrlrsdttvyycaar 117
QY 61 SAQKFGGRVSIITADESASTAYMELSLRSEDFTAIYYCAK 99
Query Match 51.4%; Score 470; DB 5; Length 143;
Best Local Similarity 56.9%; Pred. No. 1.12e-84;
Matches 74; Conservative 23; Mismatches 29; Indels 4; Gaps 4;
Db 16 qtqlv-qsgaevkpgasvkskasytftqymhvwirgagpggglewmglnpsggsts 74
QY 1 EVOLLEQSGAEVKKPGSSVKVSKASGGTFSGHVSWVRQAPGQGLEWMGGSISFFGTSN 60
Db 75 yprfgrvtrtdstsvymelsrlrsdttvyycaar 133
QY 61 SAQKFGGRVSIITADESASTAYMELSLRSEDFTAIYYCAKDPPTSGGNCYP-GF-PQOW 118
Query Match 52.3%; Score 479; DB 5; Length 117;
Best Local Similarity 70.7%; Pred. No. 7.49e-87;
Matches 70; Conservative 11; Mismatches 17; Indels 1; Gaps 1;
Db 20 qvqlv-qsgaevkpgasvkskasytftqymhvwirgagpggglewmglnpsggsts 78
QY 1 EVOLLEQSGAEVKKPGSSVKVSKASGGTFSGHVSWVRQAPGQGLEWMGGSISFFGTSN 60
Db 79 yaqkfgrvtrtdstsvymelsrlrsdttvyycaar 117
QY 64 SAQKFGGRVSIITADESASTAYMELSLRSEDFTAIYYCAK 99

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DR PIR: A02022: GLMSAA.
 DR HSSP: P01772: 1FCV
 KW IMMUNOGLOBULIN V REGION: ANTIARSONATE ANTIBODY
 FT NON_TER 114
 SQ SEQUENCE 114 AA: 12555 MW: 1A027F1D CPC32.

Query Match 47.5%; Score 435; DB 5; Length 114;
 Best Local Similarity 67.0%; Pred. No. 2 89a-76;
 Matches 71; Conservative 19; Mismatches 12; Indels 4; Gaps 4.

Db 1 evql-qsgaelvkgagsvkmsckatgytfssylywvrgapggldly-gissssayp 58
 QY 1 EVQLLEQSGAEVKKPGSSVKVSKASGCTFSGHVISWVPQAPGGLWMGGGISFFGT-S 59

Db 59 nyakfgqrvtitadestntaymelslrsdsatvycavvisry 104
 QY 60 NSAKFGQSVSITADESASTAYMELSLPSEDTAIYVCA-KDPPFF 104

RESULT 6
 ID HV1F_HUMAN STANDARD: PRT: 125 AA
 AC P06326;
 DT 01-JAN-1988 (REL. 06, CREATED)
 DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
 DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-I REGION (MOT).
 OS HOMO SAPIENS (HUMAN).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.

DR MEDLINE: 86203277.
 RA KOJIMA M., KOIDE T., ODANI S., ONO T.;
 PL MOL. IMMUNOL. 23:169-174(1986).

DR PIR: A02025: HVHMO
 DR HSSP: P01772: 8FAB
 KW IMMUNOGLOBULIN V REGION
 FT DOMAIN 1 98 V SEGMENT.
 FT DOMAIN 99 107 D SEGMENT.
 FT DOMAIN 108 125 J SEGMENT.
 FT DISULFID 22 96 HY SIMILARITY.
 FT NON_TER 125 125
 SQ SEQUENCE 125 AA: 13573 MW: 5745023 CPC32.

Query Match 47.1%; Score 431; DB 5; Length 125;
 Best Local Similarity 49.2%; Pred. No. 2 62a-75;
 Matches 63; Conservative 26; Mismatches 36; Indels 3; Gaps 3;

Db 1 qvqlv-qsgaelvkgagsvkmsckatgytfssylywvrgapggldly-gissssayp 59
 QY 1 EVQLLEQSGAEVKKPGSSVKVSKASGCTFSGHVISWVPQAPGGLWMGGGISFFGT-S 60

Db 60 ygrsqarftvtrdsstttvymetalisatdaiyycarga-hysdtdsgtsl-gpwgg 117
 QY 61 SAAKFGQSVSITADESASTAYMELSLPSEDTAIYVCAKDPPEFCSGN:YPCFFQWQ 120

Db 118 gtlvlvss 125
 QY 121 GTLVTVSS 128

RESULT 7
 ID HV02_MOUSE STANDARD: PRT: 140 AA.
 AC P01746;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).

OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-A/J;
 RX MEDLINE: 82152818
 PA SIMS J., BARBITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
 PA CAPPA J.D.;
 PL SCIENCE 256:300-311(1982);
 DR EMBL: J00493; G195007; -;
 DR PIR: A02028; HVMSG7.
 DR HSSP: P01789; 6FAB
 KW IMMUNOGLOBULIN V REGION: ANTIARSONATE ANTIBODY. HYBRIDOMA. SIGNAL.
 FT SIGNAL 1 19
 FT CHAIN 20 140 IG HEAVY CHAIN V REGION (93G7).
 FT NON_TER 140 140
 SQ SEQUENCE 140 AA: 15514 MW: 07000508 CPC32;

Query Match 46.8%; Score 428; DB 5; Length 140;
 Best Local Similarity 54.7%; Pred. No. 1 37a-74;
 Matches 70; Conservative 27; Mismatches 24; Indels 7; Gaps 6;

Db 20 evql-qsgaelvragsvkmsckatgytfssylywvrgapggldly-gissssayp 78
 QY 1 EVQLLEQSGAEVKKPGSSVKVSKASGCTFSGHVISWVPQAPGGLWMGGGISFFGT-S 60

Db 79 yrekfkgkttltvdkssstajmqlsltsodsavvfcar--shyy-ggs-y-df-dywgq 132
 QY 61 SACKFGQSVSITADESASTAYMELSLPSEDTAIYVCAKDPPEFCSGN:YPCFFQWQ 120

Db 133 gtlvtvss 140
 QY 121 GTLVTVSS 128

RESULT 8
 ID HV03_MOUSE STANDARD: PRT: 120 AA
 AC P01747;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (36-65).

OS MUS MUSCULUS (MOUSE).
 CC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 CC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.

DR MEDLINE: 83131846.
 RA SIEKEVITZ M., GEETTER M.L., BRODIE P., PIRLET P.,
 RA MAPSHAK, POTSTEIN A.;
 PL Exp. J. IMMUNOL. 12:1023-1032(1982).

CC - FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
 CC THAT HYBRIDIZE TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF
 CC THESE V REGIONS HAVE BEEN REARRANGED TO THE SAME J SEGMENT, JH2.

DR PIR: A02024: HVMSG7
 DR HSSP: P01789; 6FAB.
 KW IMMUNOGLOBULIN V REGION: ANTIARSONATE ANTIBODY. HYBRIDOMA.
 FT NON_TER 120 120
 SQ SEQUENCE 120 AA: 13307 MW: BSA00CAL CPC32;

Query Match 46.6%; Score 426; DB 5; Length 120;
 Best Local Similarity 53.5%; Pred. No. 4 11e-74;
 Matches 68; Conservative 20; Mismatches 23; Indels 7; Gaps 6;

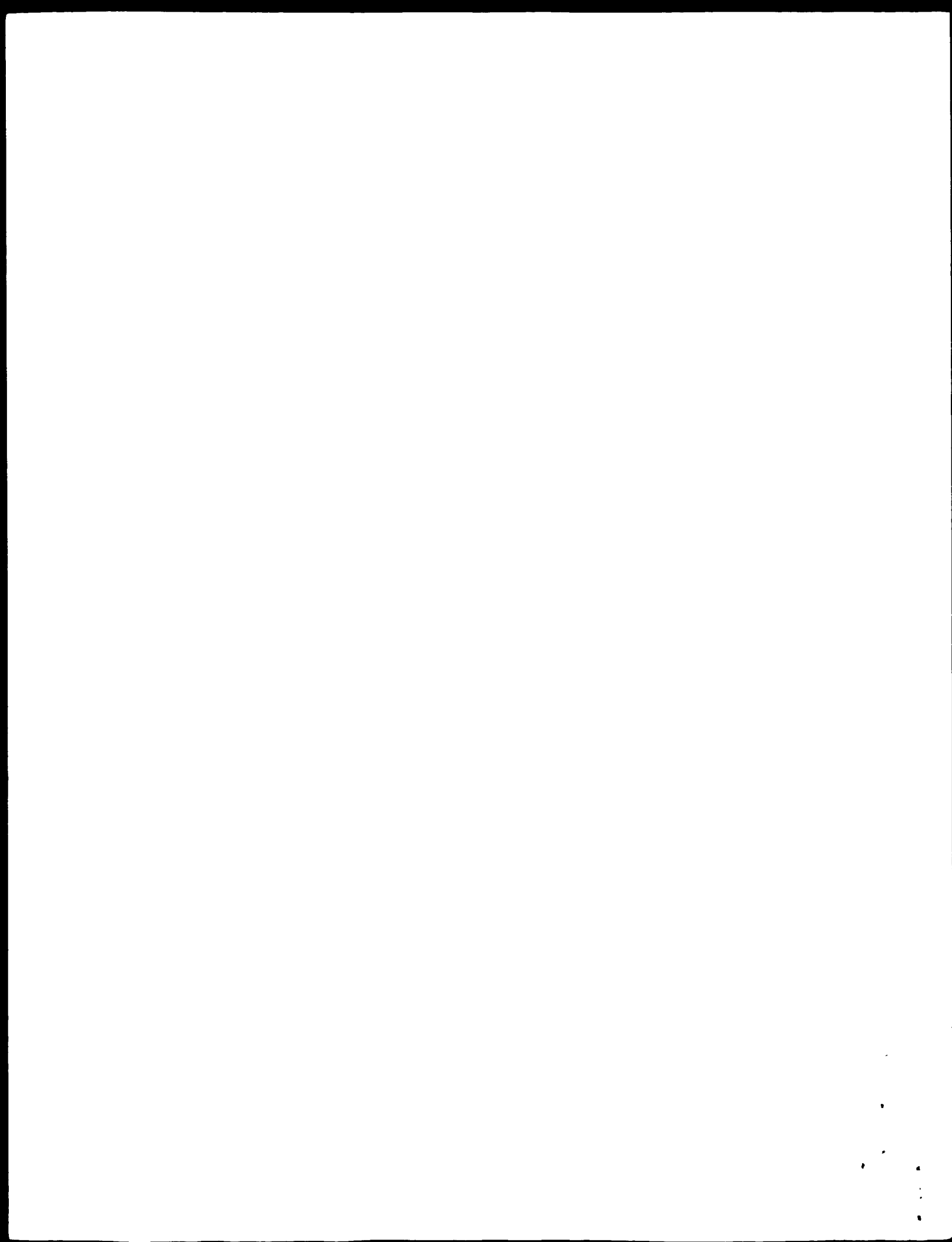
Db 1 vql-qsgaelvragsvkmsckatgytfssylywvrgapggldly-gissssayp 59
 QY 2 VALLEQSGAEVKKPGSSVKVSKASGCTFSGHVISWVPQAPGGLWMGGGISFFGT-S 61

Db 60 nekfkagkttltvdkssstajmqlsltsodsavvfcar-sv-y-y-ggs-y-y-fdywgq 113
 QY 62 AKKFGQSVSITADESASTAYMELSLPSEDTAIYVCAKDPPEFCSGN:YPCFFQWQ 121

Db 114 tltvtvss 120
 QY 122 TLTVTVSS 128

QY •1 EVQLLQSGAEVVKPGSSVKVKASGGTFSGHVSWVRQAPGQGLFWMGCSISFFFTSN 60

[illegible]



WQSELEH

(TW)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:07:23 1998; MasPar time 8.32 Seconds
468.768 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-3
Description: (1-128) from US08844215.pep
Perfect Score: 915
Sequence: 1 EVQLLEQSGAEVKKPKQSSVK NYPGFPQWGGTLTVSS 128

Scoring table: PAM 150
Gap 11

Searched: 95051 seqs, 30459580 residues

Post-processing: Minimum Watch 0%
Listing first 45 summaries

Database: p1r53
1:ann1 2:ann2 3:ann3 4:ann4 5:unann1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann11 16:unann12 17:unann18:unrev

Statistics: Mean 40.399; Variance 101.115; scale 0.400

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred. No.
1	696	76.1	125	7	Ig heavy chain V reg	9.07e-92
2	641	70.1	128	7	Ig heavy chain V reg	9.16e-83
3	637	69.5	129	7	Ig heavy chain V-1 r	4.12e-82
4	635	69.4	127	7	Ig heavy chain V reg	8.73e-82
5	633	69.2	126	7	Ig heavy chain V-1 r	1.85e-81
6	625	68.3	135	7	Ig heavy chain V reg	3.74e-80
7	624	68.2	132	7	Ig heavy chain V reg	5.44e-80
8	614	67.1	132	7	Ig heavy chain V reg	2.32e-78
9	611	66.8	133	7	Ig heavy chain V-1 r	7.13e-78
10	610	66.7	120	7	Ig mu chain precursor	7.13e-78
11	610	66.7	120	7	Ig heavy chain V reg	1.04e-77
12	609	66.6	121	7	Ig heavy chain V reg	1.51e-77
13	605	66.1	116	7	Ig heavy chain V reg	6.76e-77
14	603	65.9	116	7	Ig heavy chain V reg	1.43e-76
15	601	65.7	122	7	Ig heavy chain V reg	3.02e-76
16	601	65.7	136	7	Ig heavy chain V reg	9.29e-76
17	598	65.4	160	7	anti-pp2 erythrocyte	9.29e-76
18	594	64.9	98	7	Ig heavy chain V reg	4.15e-75
19	594	64.9	116	7	Ig heavy chain precursor	4.15e-75
20	594	64.9	119	7	Ig heavy chain V reg	4.15e-75

21	594	64.9	119	7	S44106	Ig heavy chain V-D-J	4.15e-75
22	594	64.9	123	7	S44108	Ig heavy chain V reg	4.15e-75
23	593	64.8	122	7	S49590	Ig heavy chain V1 re	6.04e-75
24	592	64.7	199	7	S24590	Ig heavy chain V reg	8.78e-74
25	587	64.2	113	7	PH1663	Ig heavy chain V reg	5.69e-74
26	583	63.7	129	7	S36290	Ig heavy chain V reg	2.54e-73
27	575	62.8	123	7	D33548	Ig heavy chain V-1 r	5.04e-72
28	572	62.5	135	7	S32374	Ig heavy chain precursor	1.54e-71
29	560	61.2	98	7	S46463	Ig heavy chain V1 re	1.36e-69
30	554	60.5	122	7	S49590	Ig heavy chain V reg	1.27e-68
31	553	60.4	117	2	G1HUED	Ig heavy chain V-1 r	1.84e-68
32	550	60.1	129	7	S46393	Ig heavy chain V reg	5.16e-68
33	549	60.0	97	7	PH0870	Ig heavy chain V reg	8.15e-68
34	549	60.0	131	7	S21924	Ig heavy chain V reg	8.15e-68
35	547	59.8	108	7	PH1664	Ig heavy chain V reg	1.71e-67
36	544	59.5	122	7	S36271	Ig heavy chain V reg	5.23e-67
37	539	58.9	99	7	A30523	Ig heavy chain V-1 r	3.36e-66
38	537	58.7	119	7	F49590	Ig heavy chain V reg	7.06e-66
39	536	58.6	124	7	S19665	Ig heavy chain V reg	1.02e-65
40	532	58.1	116	7	S31667	Ig heavy chain V reg	4.52e-65
41	525	57.4	148	7	S29257	Ig heavy chain V reg	6.97e-64
42	523	57.2	109	7	PH1621	Ig heavy chain V reg	1.27e-63
43	519	56.7	142	7	A32483	Ig heavy chain V reg	5.61e-63
44	514	56.2	118	7	S36285	Ig heavy chain V reg	3.57e-62
45	511	55.8	126	7	144151	Ig heavy chain V reg	1.09e-61

ALIGNMENTS

RESULT	1	PH0957	#type fragment	Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
ENTRY		PH0957	#formal name Homo sapiens #common name man	17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
ORGANISM		PH0957	#molecule_type DNA	16-Aug-1996
DATE		PH0957	#residues	1-125 #label MAR
ACCESSIONS		PH0957	#superfamily immunoglobulin V region, immunoglobulin homology heterotetramer; immunoglobulin	
REFERENCE		PH0957	#region framework 1\	#region framework 1\
Authors		Martin, T. J. Duffy, S. P. Carson, D. A. Kipps, T. J.	#region complementarity-determining 1\	#region complementarity-determining 1\
Journal		J. Exp. Med. (1992) 175:983-991	#region framework 2\	#region framework 2\
Title		Evidence for somatic selection of natural autoantibodies	#region complementarity-determining 2\	#region complementarity-determining 2\
#cross-references		MUID:92202880	#region framework 3\	#region complementarity-determining 3
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KEYWORDS			#domain immunoglobulin homology #label IMM\	#domain immunoglobulin homology
FEATURE			#region complementarity-determining 1\	#region complementarity-determining 1\
1-30			#region framework 2\	#region framework 2\
15-98			#region complementarity-determining 2\	#region complementarity-determining 2\
31-35			#region framework 3\	#region complementarity-determining 3
36-50			#region complementarity-determining 3	#region complementarity-determining 3
51-67			#length 125 #checksum 8143	
58-98				
99-113				
SUMMARY				
Query Match			76.1%; Score 696; DB 7; Length 125;	
Best Local Similarity			79.1%; Proj No. 9.07e-92;	
Matches			102, Conservative 14, Mismatches 8, Indels 5, Gaps 3;	
Db	1	qvqiv-qsgaevkpgsvksksggtfssvaynwrgapqgglewmgqilpigtan	59	
Qy	1	EVQLLEQSGAEVKKPKQSSVKSGKASGTTSGHVISWVPQAPQGLEWMSGISFFFTSN	60	
Db	60	yagkfqrvtitadesntatymelsslrdsdtavvyqardg---csggcyfygwfdpwg	116	
Qy	61	SAQRFQPVSTAIASASTAYMELSSLPSTAIYCAKDPFPFCGSGNCPY-GFTQQWG	119	
Db	117	qgtltvtvss	125	
Qy	120	QGTLTVTSS	128	

```

ENTRY          PH0952      #type fragment
TITLE          Ig heavy chain V region (Cδ+ CIL-SM) - human (fragment)
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
               16-Aug-1996
ACCESSIONS     PH0952
REFERENCE      Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#authors      J. Exp. Med. (1992) 175:983-991
#journal      Evidence for somatic selection of natural autoantibodies.
#title        cross-references MUID:92202880
#accesion     PH0952      nucleic acid sequence not shown
#status       PH0952
##astatus
##molecule_type DNA
##residues    1-128 ##label MAP
ORIGIN         #superfamily immunoglobulin V region; immunoglobulin homology
                heterotetramer; immunoglobulin
KEYWORDS       #region framework 1\
                #domain immunoglobulin homology #label IMM\
                #region complementarity-determining 1\
                #region framework 2\
                #region complementarity-determining 2\
                #region framework 3\
                #region complementarity-determining 3
                #length 128 #checksum 3537
FEATURE        1-30
              15-98
              31-35
              36-50
              51-67
              68-98
              99-116
SUMMARY
Query Match      70.1%; Score 641, DB 7, Length 128;
Best Local Similarity 73.6%; Pred. No. 9,16e-83;
Matches 95; Conservative 14; Mismatches 18, Indels 2, Gaps 2;

Db   1 qvqlv-qsgaeavkpgssvkysckasgdtfsyaiswvrqapggglwmggiipigtan 59
QY   1 EVQLLEQSGAEVKKPGSSVKYSCKASGDTFSGHVISWVRAPGGGLWMGGSIISFTGTN 60
Db   60 yaqkgqrvtitadtktstamylsslrsedtavvygcargnydiwgsvyrnsndafdwg 119
QY   61 SAQKFGGRVSITADEASTAYVELSLSPSEPTAIYYCAKPDP-PFCSGNGCYPCFFQQWG 119
Db   120 qgtmtvtvs 128
QY   120 QGTLVTVS 128

ENTRY          3
ENTRY          A33548      #type complete
TITLE          Ig heavy chain v-l region (NEI) - human
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
               16-Aug-1996
ACCESSIONS     A33548
REFERENCE      Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
#authors      Carson, D.A.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title        Developmentally restricted immunoglobulin heavy chain
                variable-region gene expressed at high frequency in chronic
                lymphocytic leukemia.
cross-references MUID:89345575
#accesion     A33548
#status       preliminary; not compared with conceptual translation
##molecule_type mRNA
##residues    1-129 ##label KIP
REFERENCE      PH0952
#authors      Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal      J. Exp. Med. (1992) 175:983-991
#title        Evidence for somatic selection of natural autoantibodies.
cross-references MUID:92202880
#accesion     PH0956
#status       nucleic acid sequence not shown
##molecule_type DNA
```

```

RESULT 5
ENTRY B33548 #type complete
TITLE Ig heavy chain V-1 region (AND) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996

ACCESSIONS B33548
REFERENCE Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
          Carson, D.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin heavy chain
          variable region gene expressed at high frequency in chronic
          lymphocytic leukemia.
#cross-references MUID:89345575
#accession B33548
#status preliminary; nucleic acid sequence not shown; not
          compared with conceptual translation
#molecule_type DNA
#residues 1-126 #label KIP
#experimental_source the sequence was determined from the
          differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
SUMMARY #length 126 #molecular_weight 13710 #checksum 4068

Query Match 69.2%; Score 533; DB 7; Length 126;
Best Local Similarity 74.2%; Pred. No. 1,856-81;
Matches 95; Conservative 14; Mismatches 17; Indels 2; Gaps 2;

Db 1 qvqlv-qsgaevkpkssvksskaggtfssyaiswvraqpgqglewmgiipifgtan 59
QY 1 EVQLLESGAEVKKPKSSVKVSKASGGTFSGHVTSWVPQAPQGLEWMGGSISPFGTSN 60
60 yaqkfgrvtitadeststymelsslrsoedtavyyccar-vsfgr-vqhyvyyymdvgl 119
QY 61 SAQKFGQPSVITADEASATAYMELSLPSLEDAIYYCAKDPKPPSSSNCYSPQQLWQ 120
119 qttvtvss 126
121 GTLVTVSS 128

RESULT 6
ENTRY PH0953 #type fragment
TITLE Ig heavy chain V region (G6+ CLL-SIC) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996

ACCESSIONS PH0953
REFERENCE Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession PH0953
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-135 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30 #region framework 1\
15-98 #domain immunoglobulin homology #label IMM\
31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
99-123 #region complementarity-determining 3

Db 1 qvqlv-qsgaevkpkssvksskaggtfssyaiswvraqpgqglewmgiipifgtan 59
QY 1 EVQLLESGAEVKKPKSSVKVSKASGGTFSGHVTSWVPQAPQGLEWMGGSISPFGTSN 60
60 yaqkfgrvtitadeststymelsslrsoedtavyyccar-phasididfwgvyvyygm 119
QY 61 SAQKFGQPSVITADEASATAYMELSLPSLEDAIYYCAKDPKPPSSSNCYSPQQLWQ 115
115 qttvtvss 126
121 GTLVTVSS 128

RESULT 7
ENTRY PH0954 #type fragment
TITLE Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996

ACCESSIONS PH0954
REFERENCE Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession PH0954
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-132 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30 #region framework 1\
15-98 #domain immunoglobulin homology #label IMM\
31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
99-120 #region complementarity-determining 3

Db 1 qvqlv-qsgaevkpkssvksskaggtfssyaiswvraqpgqglewmgiipifgtan 59
QY 1 EVQLLESGAEVKKPKSSVKVSKASGGTFSGHVTSWVPQAPQGLEWMGGSISPFGTSN 60
60 yaqkfgrvtitadeststymelsslrsoedtavyyccar-phasididfwgvyvyygm 119
QY 61 SAQKFGQPSVITADEASATAYMELSLPSLEDAIYYCAKDPKPPSSSNCYSPQQLWQ 115
115 qttvtvss 126
121 GTLVTVSS 128

RESULT 8
ENTRY S46394 #type complete
TITLE Ig heavy chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
23-May-1997

ACCESSIONS S46394
REFERENCE Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
#journal J. Mol. Biol. (1994) 239:68-78
#title In vitro assembly of repertoires of antibody chains on the
          surface of phage by renaturation.
#accession S46394

```

SUMMARY #length 135 #checksum 2318

```

Query Match 68.3%; Score 625; DB 7; Length 135;
Best Local Similarity 79.5%; Pred. No. 3,746-80;
Matches 89; Conservative 14; Mismatches 5; Indels 4; Gaps 3;

Db 1 qvqlv-qsgaevkpkssvksskaggtfssyaiswvraqpgqglewmgiipifgtan 59
QY 1 EVQLLESGAEVKKPKSSVKVSKASGGTFSGHVTSWVPQAPQGLEWMGGSISPFGTSN 60
60 yaqkfgrvtitadeststymelsslrsoedtavyyccarng--yo-ggdcys 108
QY 61 SAQKFGQPSVITADEASATAYMELSLPSLEDAIYYCAKDPKPPSSSNCYSPQQLWQ 112
112 qttvtvss 132

RESULT 9
ENTRY PH0954 #type fragment
TITLE Ig heavy chain V region (G6+ CLL-HEN) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996

ACCESSIONS PH0954
REFERENCE Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession PH0954
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-132 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30 #region framework 1\
15-98 #domain immunoglobulin homology #label IMM\
31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
99-120 #region complementarity-determining 3

Db 1 qvqlv-qsgaevkpkssvksskaggtfssyaiswvraqpgqglewmgiipifgtan 59
QY 1 EVQLLESGAEVKKPKSSVKVSKASGGTFSGHVTSWVPQAPQGLEWMGGSISPFGTSN 60
60 yaqkfgrvtitadeststymelsslrsoedtavyyccar-phasididfwgvyvyygm 119
QY 61 SAQKFGQPSVITADEASATAYMELSLPSLEDAIYYCAKDPKPPSSSNCYSPQQLWQ 115
115 qttvtvss 132
121 GTLVTVSS 128

RESULT 10
ENTRY S46394 #type complete
TITLE Ig heavy chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
23-May-1997

ACCESSIONS S46394
REFERENCE Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
#journal J. Mol. Biol. (1994) 239:68-78
#title In vitro assembly of repertoires of antibody chains on the
          surface of phage by renaturation.
#accession S46394

```

```

##status preliminary
##molecule_type DNA
##residues 1-132 ##label FIG
##cross-references EMBL:231681
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 132 #molecular-weight 14293 #checksum 7515

Query Match
Best Local Similarity 72.2%; Pred. No. 2,32e-78;
Matches 96; Conservative 17; Mismatches 14; Indels 6; Gaps 5;

Db 1 qvqlv-qsgaevkpgssvkscasgtfssyaiswvraqpgqglewmqgllpifgtan 59
QY 1 EVQLLEQSGAEVKKPGSSVKVKSCASGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
60 haqkfgrvtitadeststymelsslrdsstavyycartqlpaadtqilewlpssyyym 119
QY 61 SAQKFGQGRVSIADESAAYMELSLRSEDATYYCAKDP--PRFCSGG--NCYPGFF--Q 116
120 dvwqgkatmtvss 132
QY 117 Q-WGQGGLTVTVSS 128

RESULT 9
ENTRY C33548 #type complete
TITLE Ig heavy chain V-1 region (783) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996
ACCESSIONS C33548
REFERENCE A33548
#authors Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
#cross-references MUID:89345575
#accession C33548
#status preliminary; nucleic acid sequence not shown; not compared with conceptual translation
##molecule_type DNA
##residues 1-133 ##label KIP
##experimental_source the sequence was determined from the differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 133 #molecular-weight 14320 #checksum 1289

Query Match
Best Local Similarity 73.9%; Pred. No. 7.13e-78;
Matches 99; Conservative 12; Mismatches 16; Indels 7; Gaps 5;

Db 1 qvqlv-qsgaevkpgssvkscasgtfssyaiswvraqpgqglewmqgllpifgtan 59
QY 1 EVQLLEQSGAEVKKPGSSVKVKSCASGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
60 yaqkfgrvtitadeststymelsslrdsstavyycartqilgpysswypnsdyyyg 119
QY 61 SAQKFGQGRVSIADESAAYMELSLRSEDATYYCAKDP--PRFCSGG--GNC-YPGF- 114
120 mdvqgqgtvtvss 133
QY 115 FQWGGGGLTVTVSS 128

RESULT 10

```

```

ENTRY S14683 #type complete
TITLE Ig mu chain precursor; membrane bound (clone 201) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
16-Aug-1996
ACCESSIONS S14683; S08047
REFERENCE S14683
#authors Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
#journal Nucleic Acids Res. (1990) 18:4278
#title Complete nucleotide sequence of the membrane form of the human IGM heavy chain.
#cross-references MUID:90332450
#accession S14683
##molecule_type mRNA
##residues 1-627 ##label FRI
##cross-references EMBL:X17115
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS immunoglobulin, membrane protein
FEATURE
1-15 #domain signal sequence #status predicted #label SIGN
16-627 #product Ig mu chain #status predicted #label MAIN
34-117 #domain immunoglobulin homology #label IMM
SUMMARY #length 627 #molecular-weight 68510 #checksum 8581

Query Match 66.8%; Score 611; DB 7; Length 627;
Best Local Similarity 73.9%; Pred. No. 7.13e-78;
Matches 99; Conservative 12; Mismatches 16; Indels 7; Gaps 5;

Db 20 qvqlv-qsgaevkpgssvkscasgtfssyaiswvraqpgqglewmqgllpifgtan 78
QY 1 EVQLLEQSGAEVKKPGSSVKVKSCASGTFSGHVISWVRQAPGQGLEWMGGSISFFGTSN 60
60 yaqkfgrvtitadeststymelsslrdsstavyycartqilgpysswypnsdyyyg 138
QY 61 SAQKFGQGRVSIADESAAYMELSLRSEDATYYCAKDP--PRFCSGG--GNC-YPGF- 114
120 mdvqgqgtvtvss 152
QY 115 FQWGGGGLTVTVSS 128

RESULT 11
ENTRY PH0962 #type fragment
TITLE Ig heavy chain V region (66+ T-142) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0962
REFERENCE PH0962
#authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural antinodies.
#cross-references MUID:92202880
#accession PH0962
#status nucleic acid sequence not shown
##molecule_type DNA
##residues 1-120 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30 #region framework 1N
15-98 #domain immunoglobulin homology #label IMM
31-35 #region complementarity-determining 1N
36-50 #region framework 2N
51-67 #region complementarity-determining 2N
68-98 #region framework 3N
99-108 #region complementarity-determining 3
SUMMARY #length 120 #checksum 5559

Query Match 66.7%; Score 610; DB 7; Length 120;
Best Local Similarity 76.6%; Pred. No. 1.04e-77;
Matches 98; Conservative 12; Mismatches 10; Indels 8; Gaps 5;

```



```

Db 1 qvqlv-qsgaevkpgssvkscasqgtfssyaiswvraqqagqlwmggllpifqtan 59
    :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLEQSGAEVKKPGSSVKSCASGTFSSHVLSWVRAQAGGLEWMGSSISFFGISN 60
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 yackfggrvtitadeststymelsslsrsdtavvyccargv...ag-r--p-hfdwygg 112
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SACKFGGRVSIADSASTAYMELSSLSRSDTAIYCAKDPDPFPCSGNCNYPGFCQWGO 120
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 113 gtlvtvss 120
    :|||||:
QY 121 gtlvtvss 128

RESULT 12
ENTRY A49590 #type fragment
TITLE Ig heavy chain V region (ACHSV1, clone 15) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
23-May-1997
ACCESSIONS A49590
REFERENCE Burionio, R.; Williamson, R.A.; Sanna, P.P.; Bloom, F.E.;
Burton, D.F.
#journal Proc. Natl. Acad. Sci. U.S.A. (1994) 91:355-359
#title Recombinant human Fab to glycoprotein D neutralizes
infectivity and prevents cell-to-cell transmission of
herpes simplex viruses 1 and 2 in vitro.
#cross-references WU:04105168
#accession A49590
#status preliminary; not compared with conceptual translation
#molecule_type nucleic acid
#residues 1-121 #label BUR
#cross-references NCBI:P141850
#experimental_source bone marrow lymphocytes
#note #note sequence extracted from NCBI backbone
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
11-94 #domain immunoglobulin homology #label IMM
11-94 #length 121 #checksum 5226
SUMMARY

Query Match 66.6%; Score 603; DR 7; Length 121;
Best Local Similarity 71.3%; Pred. No. 1.51e-77;
Matches 87; Conservative 15; Mismatches 18; Indels 2; Gaps 2.

Db 2 esgaevkpgssvkscstsgagtsyvalnvraqagqlwmggllpifqtan 61
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 7 QSGAEVKKPGSSVKSCASGTFSSHVLSWVRAQAGGLEWMGSSISFFGISNAKPF 66
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 grvtitadeststymelsslsrsdtavvyccargv...g-cstngcslgmdvwyggttvi 119
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 67 GRVSIADSASTAYMELSSLSRSDTAIYCAKDPDPFPCSGNCNYPGFCQWGGTIVT 126
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 ss 121
    :||
QY 127 ss 128

RESULT 13
ENTRY S36261 #type fragment
TITLE Ig heavy chain V region (clone alpha-TNF-E7) - human
(fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996
ACCESSIONS S36261
REFERENCE Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Pye, J.M.;
Embleton, M.J.; McCafferty, J.; Raier, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.P.; Winter,
G.
#journal EMBO J. (1993) 12:725-734
#title Human anti-self antibodies with high specificity from phage

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#accession S36261
#status preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues 1-116 #label GRI
#cross-references EMBL:Z18841
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98 #domain immunoglobulin homology #label IMM
15-98 #length 116 #checksum 7971
SUMMARY

Query Match 66.1%; Score 605; DR 7; Length 116;
Best Local Similarity 82.5%; Pred. No. 6.76e-77;
Matches 85; Conservative 11; Mismatches 6; Indels 1; Gaps 1.

Db 1 qvqlv-qsgaevkpgssvkscasqgtfssyaiswvraqqagqlwmggllpifqtan 59
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLEQSGAEVKKPGSSVKSCASGTFSSHVLSWVRAQAGGLEWMGSSISFFGISN 60
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 yackfggrvtitadeststymelsslsrsdtavvyccargplr 102
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SACKFGGRVSIADSASTAYMELSSLSRSDTAIYCAKDPDPF 103
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
ENTRY PH0959 #type fragment
TITLE Ig heavy chain V region (G6-T-126) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0959
REFERENCE Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references NCID:92202880
#accession PH0959
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-116 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30 #region framework 1\
15-28 #domain immunoglobulin homology #label IMM
31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
99-104 #region complementarity-determining 3
SUMMARY #length 116 #checksum 5596

Query Match 65.9%; Score 603; DR 7; Length 116;
Best Local Similarity 81.7%; Pred. No. 1.43e-76;
Matches 85; Conservative 11; Mismatches 7; Indels 1; Gaps 1.

Db 1 qvqlv-qsgaevkpgssvkscasqgtfssyaiswvraqqagqlwmggllpifqtan 59
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLLEQSGAEVKKPGSSVKSCASGTFSSHVLSWVRAQAGGLEWMGSSISFFGISN 60
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 yackfggrvtitadeststymelsslsrsdtavvyccargdnwf 103
    :||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SACKFGGRVSIADSASTAYMELSSLSRSDTAIYCAKDPDPF 104
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RESULT 15
ENTRY PH0958 #type fragment
TITLE Ig heavy chain V region (G6-T-126) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0958

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REFERENCE
#authors      Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal      J. Exp. Med. (1992) 175:983-991
#title        Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:92202880
#accession    PH0958
               #status      nucleic acid sequence not shown
               #molecule_type DNA
               #residues     1-122 ##label MAR
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15-98          #domain immunoglobulin homology #label IMM\
31-35          #region complementarity-determining 1\
36-50          #region framework 2\
51-67          #region complementarity-determining 2\
68-98          #region framework 3\
99-110         #region complementarity-determining 3
SUMMARY        #length 122 #checksum 7292

Query Match      65.7%; Score 601; DB 7; Length 122;
Best Local Similarity 82.9%; Pred. No. 3.02e 76;
Matches 87; Conservative 10; Mismatches 6; Indels 2; Gaps 2;

Db      1 qqlv-qsgaevkpgssvkvskasggtfssyaiswvrqapqgglewmggiipifgtan 59
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          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          1 EVOLLEQSGAENVKPGSSVKVSKASGGTFSGHVISWVRQAPQGLEWMGGSISPFGTSN 60

Db      60 yackfgqvritadeststaymelslrsestavyycarvpnplf 104
QY      1 :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
          61 SAQKFGQRYVSIITADESASTAYWELSLRSEDTAIYYCAKDP-PRF 104

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Search completed: Tue Feb 24 07:07:53 1998
 Job time : 30 secs.

W P E R E L E

(TM)

Release 2.15 John P. Collins, BioComputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on Tue Feb 24 07:15:05 1998: MasPar time 3.28 seconds
Tabular output not generated. 198.618 Million cell updates/sec

Title: >US-08-844-215-3
Description: (1-128) from US08844215.pep
Perfect Score: 915
Sequence: 1 EVQLLEQSGAEVKKPKSSVK.....NCYPGFFQGWGGILVTVSS 128
Scoring table: PAM 150
Gap 11
Searched: 56402 seqs, 5095871 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1-back1 2.51 3 52 4 53 5 54 6 55 7 56 8 PCT00 9-PCT01
10-PCT02 11-PCT03 12-PCT04 13-PCT05 14-PCT06
Statistics: Mean 28.046; Variance 135.560; scale 0.207

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length DB ID	Description	Pred No.		
1	628	68.6	129 13	PCT-US95-0 Sequence 45, Applicati	3,600-44		
2	608	66.4	120 11	PCT-US93-1 Sequence 13, Applicati	1,930-42		
3	606	66.2	120 11	PCT-US93-1 Sequence 12, Applicati	2,880-42		
4	585	63.9	147 6	US-08-217- Sequence 4, Applicati	1,870-40		
5	560	61.2	102 10	PCT-US92-0 Sequence 55, Applicati	2,680-38		
6	560	61.2	102 10	PCT-US92-1 Sequence 63, Applicati	2,680-38		
7	560	61.2	102 10	PCT-US92-1 Sequence 63, Applicati	2,680-38		
8	560	61.2	102 7	US-07-834- Sequence 55, Applicati	5,930-38		
9	556	60.8	122 13	PCT-US95-0 Sequence 2, Applicati	1,080-37		
10	553	60.4	117 7	US-08-474- Sequence 15, Applicati	1,080-37		
11	553	60.4	117 6	US-08-477- Sequence 4, Applicati	1,080-37		
12	553	60.4	117 5	US-08-477- Sequence 15, Applicati	1,080-37		
13	553	60.4	117 6	US-08-477- Sequence 72, Applicati	1,080-37		
14	553	60.4	117 6	US-08-477- Sequence 15, Applicati	1,080-37		
15	553	60.4	117 6	US-07-634- Sequence 4, Applicati	1,080-37		
16	553	60.4	117 6	US-07-634- Sequence 72, Applicati	1,080-37		
17	553	60.4	117 6	US-07-634- Sequence 104, Applicati	1,080-37		
18	553	60.4	117 6	US-08-477- Sequence 104, Applicati	1,080-37		
19	553	60.4	117 7	US-08-487- Sequence 15, Applicati	1,080-37		
20	553	60.4	117 7	US-08-487- Sequence 72, Applicati	1,080-37		
21	553	60.4	117 7	US-08-474- Sequence 104, Applicati	1,080-37		
22	553	60.4	117 7	US-08-474- Sequence 72, Applicati	1,080-37		

ALIGNMENTS							
RESULT	ID	Sequence	Standard	PRT	AA		
1	PCT-US95-01219-45	Sequence 45, Application PC/TUS9501219.	Sequence 45, Application PC/TUS9501219.	Sequence 45, Application PC/TUS9501219.	Sequence 45, Application PC/TUS9501219.		
XX	AC	xxxxxx					
XX	DT	01-JAN-1900					
XX	DE	Sequence 45, Application PC/TUS9501219.					
XX	CC	Sequence 45, Application PC/TUS9501219					
CC	CC	GENERAL INFORMATION:					
CC	CC	APPLICANT: Pending, Mary M					
CC	CC	APPLICANT: Leger, Olivier J.					
CC	CC	APPLICANT: Saidanha, Jose					
CC	CC	APPLICANT: Jones, S. Tarran					
CC	CC	TITLE OF INVENTION: Humanized Antibodies Against Leukocyte					
CC	CC	TITLE OF INVENTION: Adhesion Molecule VLA-4					
CC	CC	NUMBER OF SEQUENCES: 45					
CC	CC	CORRESPONDENCE ADDRESS:					
CC	CC	ADDRESSEE: Townsend and Townsend Kourie and Crew					
CC	CC	STREET: One Market Plaza, Stewart Tower, Suite 2000					
CC	CC	CITY: San Francisco					
CC	CC	STATE: California					
CC	CC	COUNTRY: USA					
CC	CC	ZIP: 94105					
CC	CC	COMPUTER READABLE FORM:					
CC	CC	MEDIUM TYPE: Floppy disk					
CC	CC	COMPUTER: IBM PC compatible					
CC	CC	OPERATING SYSTEM: PC-DOS/MS-DOS					
CC	CC	SOFTWARE: Patent in Release #10, Version #1 25					
CC	CC	CURRENT APPLICATION DATA:					
CC	CC	APPLICATION NUMBER: PCT/US95/01219					
CC	CC	FILING DATE: 25-JAN-1995					
CC	CC	CLASSIFICATION:					
CC	CC	PRIOR APPLICATION DATA:					
CC	CC	APPLICATION NUMBER: US 08/196,269					
CC	CC	FILING DATE: 25-JAN-1994					
CC	CC	ATTORNEY/AGENT INFORMATION:					
CC	CC	NAME: Smith, William L.					
CC	CC	REGISTRATION NUMBER: 30,223					
CC	CC	REFERENCE/DOCKET NUMBER: 15270-14					
CC	CC	TELECOMMUNICATION INFORMATION:					
CC	CC	TELEPHONE: 415-543-9600					
CC	CC	TELEFAX: 415-543-5043					
CC	CC	INFORMATION FOR SEQ ID NO: 45:					
CC	CC	SEQUENCE CHARACTERISTICS:					

CC	TOPOLOGY:	linear	MOLECULE TYPE:	peptide
CC	TOPOLOGY:	linear	MOLECULE TYPE:	peptide
CC	TOPOLOGY:	linear	MOLECULE TYPE:	peptide

CC IMMEDIATE SOURCE:
 CC CLONE: BOR
 CC FEATURE: Peptide
 CC NAME/KEY: LOCATION: 1..120
 CC SEQUENCE 120 AA; 12984 MW; 80846 CN;

Query Match 66 24; Score 606; DR 11; Length 120;
 Best Local Similarity 74 44; Prod No 2 84a-42;
 Matches 95; Conservative 15; Mismatches 10; Indels 7; Gaps 5;

Db 1 VOLV-QSGAEVKKPGSSVVKVTKASGDTFSSAISWVRQAPGGGLEWGGIPIFGTNY 59
 QY 2 VOLV-QSGAEVKKPGSSVVKVTKASGDTFSSAISWVRQAPGGGLEWGGIPIFGTNS 61
 Db 60 AKQFGQVITTDSTAYMEVSSLPSEDTALTYCAPEGREM-AI-N-P-FDYWGQ 113
 QY 62 AKQFGQVITADESTAYMELSSLPSEDTALTYCAKDPFRFCGNGCYPGFFQWQGG 121
 Db 114 TLTVSS 120
 QY 122 TLTVSS 128

RESULT 4
 ID US-08-217-918-4 STANDARD; PPT; 147 AA.
 XX
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 4, Application US/08217918
 XX
 CC Sequence 4, Application US/08217918
 CC Patent No. 5506132
 CC GENERAL INFORMATION:
 CC APPLICANT: LAKE, PHILIP
 CC APPLICANT: OSTBERG, LARS
 CC TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
 CC TITLE OF INVENTION: VAPICELLA-ZOSTER VIRUS
 CC NUMBER OF SEQUENCES: 4
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESS: Townsend and Townsend Kourie and Crew
 CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: IBM PC compatible
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/217,918
 CC FILING DATE: 24-MAR-1994
 CC CLASSIFICATION: 530
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M
 CC REGISTRATION NUMBER: 30,223
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (415) 326-2400
 CC TELEFAX: (415) 326-2422
 CC INFORMATION FOR SEQ ID NO: 4:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 147 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 147 AA; 15801 MW; 123306 CN;

Query Match 63 48; Score 585; DR 6; Length 147;
 Best Local Similarity 70 28; Prod No 1 87a-40;

Matches 92; Conservative 15; Mismatches 18; Indels 6; Gaps 5;

Db 20 QVQLV-QSGAEVKKPGSSVVKVTKASGDTFSSAISWVRQAPGGGLEWGGIPIFGT 78
 QY 1 EVQLLESGAEVKKPGSSVVKVTKASGDTFSSAISWVRQAPGGGLEWGGIPIFGT 60
 Db 79 YAKFGUGKVTISALASTAYMELSSLPSEDTALTYCAKDPFRFCGNGCYPGFFQWQ 136
 QY 41 SAQFGQVITADESTAYMELSSLPSEDTALTYCAKDPFRFCGNGCYPGFFQWQ 117
 Db 137 WGQGTIVTVSS 147
 QY 118 WGQGTIVTVSS 128

RESULT 5
 ID PCT-US92-06185-55 STANDARD; PPT; 102 AA.
 XX
 AC xxxxxx
 DT 01-JAN-1900
 DE Sequence 55, Application PC/TUS9206185.
 XX
 CC Sequence 55, Application PC/TUS9206185
 CC GENERAL INFORMATION:
 CC APPLICANT: Lonberg, Nils
 CC APPLICANT: Kay, Robert M.
 CC TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 75
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: William M. Smith
 CC STREET: One Market Plaza, Stewart Tower, Suite 2000
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent In Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US92/06185
 CC FILING DATE: 19910828
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M.
 CC REGISTRATION NUMBER: 87654
 CC REFERENCE/DOCKET NUMBER: 14643-5
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-543-9600
 CC TELEFAX: 415-543-5043
 CC INFORMATION FOR SEQ ID NO: 55:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 102 amino acids
 CC TYPE: AMINO ACID
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE 102 AA; 10940 MW; 55781 CN;

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 Best Local Similarity 80 89; Prod No 2 68e-38;
 Matches 80; Conservative 11; Mismatches 7; Indels 1; Gaps 1;

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 QY 1 EVQLLESGAEVKKPGSSVVKVTKASGDTFSSAISWVRQAPGGGLEWGGIPIFGT 60
 Db 54 YAKFGUGKVTISALASTAYMELSSLPSEDTALTYCAKDPFRFCGNGCYPGFFQWQ 102

CC APPLICANT: Kay, Robert M
 CC TITLE OF INVENTION: Transgenic No. 553425-Human Animals Capable of
 CC TITLE OF INVENTION: Producing Heterologous Antibodies
 CC NUMBER OF SEQUENCES: 77
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: William M. Smith
 CC STREET: One Market Plaza, Stewart Tower, Suite 2000
 CC CITY: San Francisco
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 94105
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/07/834,539A
 CC FILING DATE: 19920205
 CC CLASSIFICATION: 800
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Smith, William M. 223
 CC REGISTRATION NUMBER: 30,223
 CC REFERENCE/DOCKET NUMBER: 14643-5
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 415-543-9600
 CC TELEFAX: 415-543-5043
 CC INFORMATION FOR SEQ ID NO: 55:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 102 amino acids
 CC TYPE: AMINO ACID
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC SEQUENCE: 102 AA, 10340 MW, 55761 CN

Query Match 61 24, Score 560, DB 7, Length 102,
 Best Local Similarity 80.8%, Pred. No. 2, Gap 134,
 Matches 80, Conservative 11, Mismatches 7, Indels 1, Gaps 1

Db 5 OVQLV-OSGAEVKPGSSVKSKASGGTSSVAISWVPCAPGCGLEWMPPIPIGIAN 63
 QY 1 EVQLQSGAEVKPGSSVKSKASGGTSSGHVSWVPCAPGCGLEWMPPIPIGIAN 63
 Db 64 YAKFGQGRVTITADKSTAYMELSSLSRDTAVYYCAP 102
 QY 1 EVQLQSGAEVKPGSSVKSKASGGTSSGHVSWVPCAPGCGLEWMPPIPIGIAN 63
 Db 64 YAKFGQGRVTITADKSTAYMELSSLSRDTAVYYCAP 102
 QY 1 EVQLQSGAEVKPGSSVKSKASGGTSSGHVSWVPCAPGCGLEWMPPIPIGIAN 63
 Db 64 YAKFGQGRVTITADKSTAYMELSSLSRDTAVYYCAP 102
 QY 1 EVQLQSGAEVKPGSSVKSKASGGTSSGHVSWVPCAPGCGLEWMPPIPIGIAN 63

RESULT 9
 ID PC/US95-00067-2 STANDARD: PPT: 122 AA
 XX AC xxxxxx
 XX DT 01-JAN-1990
 XX DE Sequence 2, Application PC/TUS9500067
 XX CC GENERAL INFORMATION:
 CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
 CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPPEPS
 CC TITLE OF INVENTION: SIMPLEX VIRUS AND METHODS THEREFOR
 CC NUMBER OF SEQUENCES: 25
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1880 Century Park East, Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM: disk
 CC MEDIUM TYPE: Floppy disk

CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/00067
 CC FILING DATE: 04-JAN-1995
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Halle, Ph D., Lisa A.
 CC REGISTRATION NUMBER: 38,347
 CC REFERENCE/DOCKET NUMBER: FD-3229
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO: 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 122 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: FBH5V 8
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1-122
 CC SEQUENCE: 122 AA, 12999 MW, 86543 CN

Query Match 60 84, Score 556, DB 13, Length 122,
 Best Local Similarity 56.9%, Pred. No. 5, Gap 38,
 Matches 83, Conservative 20, Mismatches 19, Indels 2, Gaps 2

Db 1 LEQSGAEVKPGSSVKSKASGGTSSVAISWVPCAPGCGLEWMPPIPIGIAN 60
 QY 5 LEQSGAEVKPGSSVKSKASGGTSSGHVSWVPCAPGCGLEWMPPIPIGIAN 64
 Db 61 FQDLITITADKSTAYMELSSLSRDTAVYYCAP-VA-YMPEPTVAGIDWGGQITV 118
 QY 65 FQDLITITADKSTAYMELSSLSRDTAVYYCAP-VA-YMPEPTVAGIDWGGQITV 124

Db 119 TVAS 122
 QY 125 TVSS 128

RESULT 10
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 XX AC xxxxxx
 XX DT 01-JAN-1990
 XX DE Sequence 15, Application US/08474040
 XX CC Sequence 15, Application US/08474040
 CC Patent No. 5693761
 CC GENERAL INFORMATION:
 CC APPLICANT: QUEEN, Cary L.
 CC APPLICANT: CO. Man Sung
 CC APPLICANT: SCHNEIDER, William P.
 CC APPLICANT: LANDOLFI, Nicholas F.
 CC APPLICANT: COELING, Kathleen L.
 CC APPLICANT: SELICK, Harold E.
 CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
 CC NUMBER OF SEQUENCES: 113
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Townsend and Townsend Kourie and Crew
 CC STREET: 379 Lytton Avenue
 CC CITY: Palo Alto
 CC STATE: California
 CC COUNTRY: US
 CC ZIP: 94301
 CC COMPUTER READABLE FORM:

CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Townsend and Townsend and Crew LLP
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent In Release #1 0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 1:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1 117
CC OTHER INFORMATION: /note="Fu heavy chain amino acid
CC OTHER INFORMATION: sequence"
SQ SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 60.4%; Score 553; DB 6; Length 117;
Best Local Similarity 80.6%; Pre-3. No. 1.08e-37;
Matches 79; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

Db 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTSPSAIIHWPAQPGGLEWMGGIVPMGPPN 59
QY 1 EVQLLESGAEVKKPGSSVKVSCKASGGTSPSAIIHWPAQPGGLEWMGGISLFGTSN 60
Db 60 YAKQFGQVRVITADESTNTAYMELSSLPSSECTAFYFCA 97
QY 61 SAQKFGQVRVITADESTNTAYMELSSLPSSECTAFYFCA 98

RESULT 13
ID US-08-477-728-72 STANDARD: PRT: 117 AA.
XX
AC xxxxxx
XX

DI 01-JAN-1990
XX Sequence 72, Application US/08477728.
DE Sequence 72, Application US/08477728
XX Patent No. 5585089
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESS: Townsend and Townsend and Crew LLP
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94111
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC compatible
CC SOFTWARE: Patent In Release #1 0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US 08/477,728
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/634,278
CC FILING DATE: 19-DEC-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 72:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
SQ SEQUENCE 117 AA; 12472 MW; 77871 CN;

Query Match 60.4%; Score 553; DB 6; Length 117;
Best Local Similarity 80.6%; Pre-3. No. 1.08e-37;
Matches 79; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

Db 1 QVQLVQSGAEVKKPGSSVKVSCKASGGTSPSAIIHWPAQPGGLEWMGGIVPMGPPN 59
QY 1 EVQLLESGAEVKKPGSSVKVSCKASGGTSPSAIIHWPAQPGGLEWMGGISLFGTSN 60
Db 60 YAKQFGQVRVITADESTNTAYMELSSLPSSECTAFYFCA 97
QY 61 SAQKFGQVRVITADESTNTAYMELSSLPSSECTAFYFCA 98

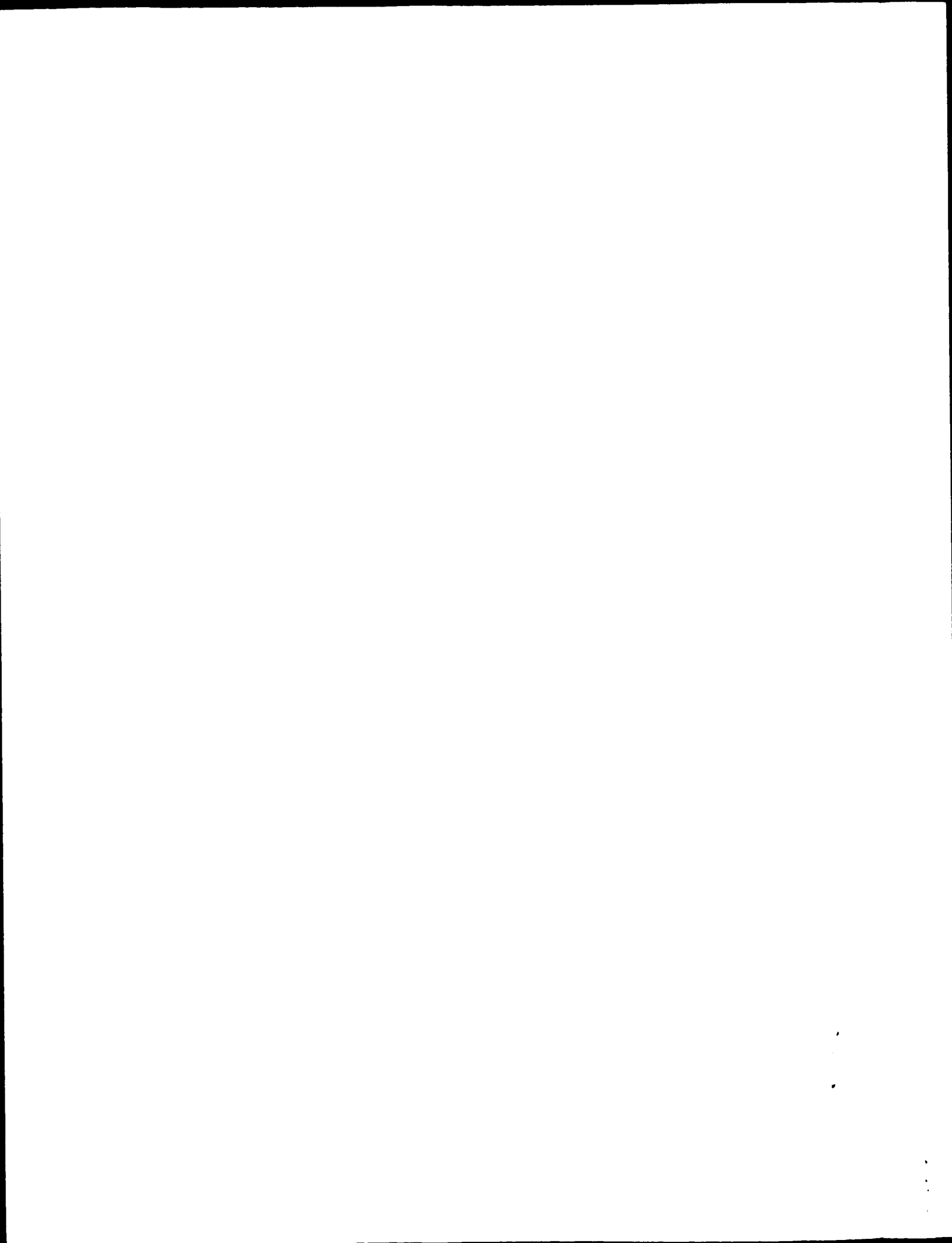
RESULT 14
ID US-07-634-278-15 STANDARD: PRT: 117 AA.
XX
AC xxxxxx
XX

XX 01-JAN-1900
DE Sequence 15, Application US/07634278.
XX Patent No. 5530101
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/634,278
CC FILING DATE: 19-DEC-1990
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO. 15:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1-117
CC OTHER INFORMATION: /note= "Eu heavy chain amino acid
CC SEQUENCE 117 AA: 12472 MW: 77871 CN;
Query Match 60.4%; Score 553; DB 6; Length 117;
Best Local Similarity 80.6%; Pred. No. 1.08e-37;
Matches 79; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
Db 1 QVQLVQSGAEVKKPKSSVKVSKASGTSRPSAITHVRCAPOGGLGFWMGCIYDMGPPN 59
QY 1 EVQLLESGAEVKKPKSSVKVSKASGTSRPSAITHVRCAPOGGLGFWMGCIYDMGPPN 60
Db 60 YAKFGQGVTTTADSESTAYMELSSLRSEDTAFYFCA 97
Matches 79; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 61 SAKFGQGVTTTADSESTAYMELSSLRSEDTAFYFCA 98
RESULT 15
ID US-07-634-278-4 STANDARD; PRT: 117 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX Sequence 4, Application US/07634278.
XX Sequence 4, Application US/07634278
CC Patent No. 5530101
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: COELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/07/634,278
CC FILING DATE: 19-DEC-1990
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 4:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC HYPOTHETICAL: NO
CC FEATURE:
CC NAME/KEY: Protein
CC LOCATION: 1-117
CC OTHER INFORMATION: /note= "Variable region of the human
CC OTHER INFORMATION: Eu antibody heavy chain."
CC SEQUENCE 117 AA: 12472 MW: 77871 CN;
Query Match 60.4%; Score 553; DB 6; Length 117;
Best Local Similarity 80.6%; Pred. No. 1.08e-37;
Matches 79; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

Db 1 QVQV-OSCAEVKKPSSSVKVSCKASGTFSPSRAIIWVQAPGQGLEWMSGIYVMPGPPN 59
QY 1 EVQLEQSGAEVKKPGSSVKVSCKASGTFSSHVISWVQAPGQGLEWMSGSIFFPGTSN 60
Db 60 YAKRFGPVTITADESTNTAYMFISSLPSEDTAFYCA 97
QY 61 SAQRFGPVTITADESTNTAYMFISSLPSEDTAFYCA 98

Search completed: Tue Feb 24 07:35:16 1998
Job time : 11 secs.



 WQESREH

 (TM)

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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:08:10 1998 MasPar time 7.03 Seconds

Tabular output not generated. 252,969 Million cell updates/sec

Title: >US-08-844-215-3
 Description: (1-128) from US08844215.pcp
 Perfect Score: 915
 Sequence: 1 EVQLLEQSGAEVKKPQGSVK NCPGPFQONGQGLVTVSS 128

Scoring table: PAM 150
 Gap 11

Searched: 111726 seqs, 13999129 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: a-geneseq30
 1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
 8:part8 9:part9 10:part10 11:part11 12:part12 13:part13
 14:part14 15:part15 16:part16 17:part17 18:part18
 19:part19 20:part20 21:part21 22:part22 23:part23

Statistics: Mean 30.241 Variance 147.704 scale 0.205
 pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query Match	Length	ID	Description	Pred. No.	
1	756	82.5	481	5	P24442 Sequence of antibody	9.75e-54	
2	608	66.4	120	9	SPA-reactive IGM heavy	4.58e-41	
3	608	66.4	476	5	Antibody D heavy chain	4.58e-41	
4	601	65.7	123	23	CEA-specific antibody	1.81e-40	
5	594	64.9	98	12	DP10 VH region	7.13e-40	
6	593	64.8	123	23	CEA-specific antibody	8.68e-40	
7	592	64.7	123	23	CEA-specific antibody	1.06e-39	
8	591	64.6	123	23	CEA-specific antibody	1.28e-39	
9	588	64.3	123	23	CEA-specific antibody	2.21e-39	
10	585	63.9	147	12	93KA9 anti-VariCella	4.16e-39	
11	584	63.8	119	23	Anti-melanoma antibody	5.06e-39	
12	578	63.2	120	9	SPA-reactive IGM heavy	1.64e-38	
13	560	61.2	109	12	HV1263 VH region	3.55e-37	
14	560	61.2	117	4	Protein encoded by th	5.55e-37	
15	560	61.2	117	7	Human heavy chain V r	5.55e-37	
16	560	61.2	117	20	DNA fragment vH49 8,	5.55e-37	
17	556	60.8	122	14	HSV-neutralising anti	1.21e-36	
18	553	60.4	122	14	Human antibody Eu hea	2.19e-36	
19	553	60.4	119	9	Heavy chain variable	2.19e-36	
20	552	60.2	124	9	Monoclonal antibody 3	3.51e-36	

21	548	59.9	102	5	P25225	HR region of human rh	5.80e-36
22	546	59.7	121	14	R77874	Humanised mouse Dpc-2	8.57e-36
23	546	59.7	140	9	P55556	DP99-200 Humanized an	8.57e-36
24	542	59.3	145	22	W22941	Human anti-tumor ant	1.54e-35
25	539	58.9	249	14	R77610	Humanised 5G1.1 VH +	3.36e-35
26	534	58.4	140	23	W21947	Humanised heavy chain	3.92e-35
27	530	57.9	142	9	P50188	Heavy chain variable	1.05e-34
28	528	57.7	249	14	R77615	Humanised 5G1.1 VH +	2.87e-34
29	524	57.3	142	9	R50134	Heavy chain variable	6.27e-34
30	521	56.9	248	14	R77616	Humanised CDP-grafted	1.11e-33
31	516	56.4	140	23	W21849	Humanised heavy chain	2.98e-33
32	515	56.3	232	7	R39267	Humanised C4G1 Ig hea	3.62e-33
33	515	56.3	235	7	R39268	Humanised C4G1 Ig hea	3.62e-33
34	515	56.3	449	7	P43339	Completely humanised	3.62e-33
35	513	56.1	121	16	P88804	VHmu for antibody RA3	5.34e-33
36	512	56.0	458	5	P28808	pre-5A8 humanised hea	5.49e-33
37	509	55.6	140	23	W21850	Humanised heavy chain	1.16e-32
38	507	55.4	142	9	P50132	Heavy chain variable	1.72e-32
39	504	55.1	123	23	W22413	Humanised alpha 4 int	3.08e-32
40	503	55.0	98	12	R73070	CP7H1.2 VH-1 H chain	2.74e-32
41	502	54.9	126	9	P45609	Monoclonal antibody G	4.54e-32
42	502	54.9	142	9	R50186	Heavy chain variable	4.54e-32
43	502	54.9	249	14	R77617	Humanised CDP-grafted	4.54e-32
44	502	54.9	249	14	R77611	Humanised 5G1.1 VH +	4.54e-32
45	500	54.6	142	15	R91332	Human VLA-4 reshaped	6.70e-32

ALIGNMENTS

RESULT 1
 ID R24442 standard; Protein: 481 AA.
 AC R24442;
 DI 02-JAN-1992 (first entry)
 DE Sequence of antibody molecule IgG1.
 KW Antibody; immunoglobulin G1.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc_difference 308
 FT /label= N
 FT /note= "Sketch for extra glycan addition site"
 FT Misc_difference 310
 FT /label= S
 FT /note= "see above"
 FT Misc_difference 321
 FT /label= N
 FT /note= "see above"
 FT Misc_difference 329
 FT /label= N
 FT /note= "see above"
 FT Misc_difference 331
 FT /label= S
 FT /note= "see above"
 FT Misc_difference 356
 FT /label= N
 FT /note= "see above"
 FT Misc_difference 369
 FT /label= N
 FT /note= "see above"
 FT Misc_difference 370
 FT /label= N
 FT /note= "see above"

PD 11-JUN-1992.
 PP 18-NOV-1991; U08605.
 PR C3-NOV-1990; US-618314.
 PA (GENO.) GEN HOSPITAL CORP.
 PI Seed B. Walz G.
 PR W21849, 218783/25.
 ER NPS22, 225443.
 FT Inhibition of cell adhesion mediated through ELAM-1 mol. binding
 FT - used in treating chronic inflammation, rheumatoid arthritis,
 FT psoriasis, etc.
 PS Disclosure; Fig. 1: 46pp; English.
 WC The 1991, in its nascent form, bears no similarity side chains. The
 CC inventors designed a molecule including several such sites for
 CC attachment of sialyl-Lex side chains (see E24442, FT). The

additional N-linked glycosylation sites are introduced at locations which impair complement fixing and Fc receptor binding ability. They are preferably located in the CH2 region of the Ig molecule. Antibodies bearing multiple stavalyl-lex determinants are useful for disrupting undesirable interactions between cells or proteins. Disrupting this interaction has therapeutic applications, for example, in minimising inflammation following tissue injury. Sequence 481 AA:

Query Match	82.6%;	Score 756;	DB 5;	Length 481;
Best Local Similarity	81.3%;	Pred. No. 9,75e-54;		
Matches	104;	Conservative	14;	Mismatches 9;
			Indels	1;
			Gaps	1;

Db	25	qvqlv-qsgaevkxpgssvkvsckasqgtfssyaiswvraqpgagqlwmgaipifqtan	83
QY	1	EVQLLESGAEVKKPGSSVKVKSCKASGGTFSCHVITSWVRQAPGGGLWMGGSISFGTSN	60
Db	84	yaqxfqrvlitaeststaymelslrsedtaavyccardngaycsggscysawfdpwq	143
QY	61	SAQFQGRVITADEASTAYMELSLRSEDTAIYYCAKDPFRCSGGNCPGFFQWQ	120
Db	144	qtlvtvs	151
QY	121	GTLTVTSS	128

RESULT	2	
ID	R54796	standard; peptide: 120 AA.
AC	R54796;	
DE	18-OCT-1994	(first entry)
DT	SpA-reactive IgM heavy chain clone KAS.	
DI	SpA domain D; Ig binding region; IgM: B-cell superantigen; sAg.	
DE	superantigen; heavy chain variable region; VH3 restricted antibody;	
KW	VH; protein-A; KAS: B-lymphocyte; vaccine.	
KW	Homo sapiens.	
OS	Os	
PN	WO9409818-A.	
PN	11-MAY-1994.	
PD	29-OCT-1993;	U10555.
PF	30-OCT-1992;	US-969936.
PR	(PEGC) UNIV CALIFORNIA.	
PA	Silverman GJ;	
PI	WPI: 94-167127/20.	
PT	Stimulating prodn. of variable region gene family restricted	
PT	antibodies - through B-cell super-antigen vaccination	
PT	Disclosure; Page 78; 130pp; English.	
PS	A B-cell superantigen (sAg) is a fragment of SpA D domain that	
CC	specifically binds the Fab portion of variable region of restricted	
CC	antibodies. The sAg is used to enhance production of VH, especially	
CC	VH3, restricted Abs. During attempts to identify sAgs, aa sequences	
CC	(R54784-801) of H chains from Ig reactive with mod-SpA, aa and	
CC	DNA sequences (R54802-16, Q64842-56) of VH regions of SpA binders	
CC	obtained from combinatorial libraries were determined. IgM protein	
CC	KAS is derived from the germline configuration of a VH gene	
CC	segment.	
SO	Sequence	120 AA;
SO		

Query Match 65.4%; Score 608; DB 9; Length 120;
Best Local Similarity 74.0%; Pred. No. 4.58e-41;
Matches 94; Conservative 15; Mismatches 11; Indels 7; Gaps 4;

Db	1	vhlv-gsaevkqasvkvscasqdtfsyaiswrcapqgdltwmqgdlipifqany	59
QY	2	vqlleqsgaevkfkpsvkvscasggtffshvswrpaqgqlwemwsgtiffgtsns	61
Db	60	aqkfgtrvltadestntaymelrsrddtamycakeq---y---gd-yurpfdfwqy	113
QY	62	aqkfcqrvsitadesastaymelsslrsestaiyycaakoppfcsgsgnc-yf-ftfwgsgq	122
Db	114	tlvtvss	120
QY	122	tlvtvss	128

RESULT	3	
ID	R31023	standard; protein: 476 AA.
AC	R31023	
DE	19-MAY-1993	(first entry)
DE	Antibody D heavy chain.	
DE	Heavy, light, chain, antibody: D; monoclonal; peripheral blood;	
DE	lymphocyte; hepatitis A virus; HAV; sero; positive; patient;	
DE	murine; B5B3; polyadenylated; cDNA library; human; kappa; L; H.	
OS	Synthetic.	
Key	Location/Qualifiers	
FT	Peptide	1..19
FT	/note= "Signal peptide"	
FT	/Region	20..49
FT	/label= FR1	
FT	/Region	50..54
FT	/label= CDR1	
FT	/Region	55..68
FT	/label= FR2	
FT	/Region	69..84
FT	/label= CDR2	
FT	/Region	85..113
FT	/label= FR3	
FT	/Region	114..121
FT	/label= CDR3	
FT	/Region	122..132
FT	/label= FR4	
FT	/Domain	133..241
FT	/label= CH1	
FT	/Region	242..262
FT	/label= HINGE	
FT	/Domain	263..379
FT	/label= CH2	
FT	/Domain	380..497
FT	/label= CH3	
PN	EP-523949-A.	
PD	20-JAN-1993.	
PF	14-JUL-1982; 306420.	
PR	15-JUL-1991; GB-015284.	
PR	01-AUG-1991; GB-016594.	
PR	23-MAR-1992; GB-006284.	
PA	(WELL) WELLCOME FOUND LTD.	
PI	Grove JS, Lewis AP;	
PI	WPI: 93-019951/03.	
DR	N-PDB: Q35099.	
PT	prodn. of recombinant primate antibodies - useful for treating	
PT	infections caused by hepatitis A, B and C, herpes,	
PT	cytomegalovirus, AIDS, ARC, also treat multiple sclerosis.	
PT	arthritis etc.	
PP	Disclosure: Fig 2: 35pp; English.	
CC	The sequences given in R31023-24 represent the heavy and light chains	
CC	of Antibody D respectively. Antibody D is a monoclonal antibody which	
CC	was derived from peripheral blood lymphocytes from a hepatitis A virus	
CC	(HAV) sero positive patient. Antibody D is closely related in nature	
CC	to murine antibody B5B3. Total RNA was isolated from antibody D	
CC	expressing cells and polyadenylated RNA was extracted. These polyA	
CC	RNA's were used to prepare a cDNA library which was screened for human	
CC	kappa light (L) chains and two positive clones were detected.	
CC	Further heavy (H) chain clones were also isolated.	
SO	Sequence 476 AA;	
SO		

```
Query Match      66.4%; Score 608; DB 6; Length 476;
Best Local Similarity 70.3%; Pred. No. 4,58e-41;
Matches          90; Conservative 15; Mismatches 22; Indels 1; Gaps 1;
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20 qmgyv-dsgacvkpkssvtv-scakggqfshyaiswvrqapqqlwmqqilptqtpt 78
:
1 EVGLSSGAFVKKFSSVPVCWKAQSGTFSHVI:SWVFAPLQL:LFWMI:SLSPRTSN 60

79 ysqnfgrvitadkstkstahmltsirsdtaavyccatdyrvrqandrarqvwdpwqj 148
:
61 SAQFGQGRVSTADESASTAYMELLSURSDTAIYCAKDPHPFTSGGNCNYCFUQWCQ 120

139 qltlvtvs 146

QY * 121 GTLTVSS 128
|||||

RESULT 4

ID W19888 standard; Protein: 123 AA.
AC W19888.
DT 07-DEC-1997 (first entry)
DE CEA-specific antibody CEA6 VH mutant HBB11 sequence.
KW Carcinoembryonic antigen; CEA; human; antibody; scfv;
KW tumour marker; lung cancer; breast cancer; colon cancer;
KW adenocarcinoma; diagnosis.
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..56
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 99..112
FT /label= CDR3
FT /note= "complementarity determining region 3"
PN WO9720932-A1.
PD 12-JUN-1997.
PF 09-DEC-1996; G03043
PF 11-OCT-1996; GB-021295.
PR 07-DEC-1995; GB-025004
PR 23-MAY-1996; GB-010824.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY
PI Allen DJ, McCafferty JG, Osbourn JK;
DR WPI: 97-319779/29.
PT Specific binding members for human carcinoembryonic antigen - bind
PT to the A3-B3 extracellular domain of hCEA and are substantially
PT non-cross-reactive with human liver cells; used for diagnosing
PT cancer
PS Claim 4; Fig 2; 128pp; English.
CC This polypeptide sequence comprises the heavy chain variable region
CC (VH), HBB11, obtained by mutagenesis of the VH CDR3 of human
CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
CC W19881). A claimed specific binding member (A) comprises an hCEA
CC specific antibody antigen binding domain that has a dissociation
CC constant for hCEA of less than 1 x 10⁻⁸ M, is non-cross-reactive
CC with human liver cells, and preferentially binds to the A3-B3
CC extracellular domain of hCEA and/or to cell-associated hCEA over
CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
CC VL sequences from CEA1-7 (see W19876-85), or their CDR sequences,
CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
CC mutagenesis or chain shuffling. An example of a claimed pairing
CC is HBB11 VH with CEA6 VL. (A) is used to detect cells expressing
CC hCEA, in vivo or in vitro, especially tumour cells for diagnosing
CC cancer, e.g. adenocarcinoma of the colon, lung or breast
SQ Sequence 123 AA.

Query Match 65.7%; Score 601; DR 23; Length 123;
Best Local Similarity 71.1%; Pred. NO. 1.81e-40;
Matches 91; Conservative 15; Mismatches 15; Indels 5; Gaps 3;

Db 1 qqlv-qsgaevkpkpssvkcsksggtfssyalswvrgapqgglewmggiipfgtan 59
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QY 1 EVCLLEQSGAEVKKPSSVKVSKASGGTFSGHVISWVPQAPQGLEWGGSIFFGTGN 60
|||||:|||||

Db 60 yaqkfgrvitadeststymelslsrdsedstavyvcarhny--elyyy--ymdvwqg 115
|||||:|||||

QY 61 SAKKFGFVSVITADESASTAYMELSLRSEDSTAYVYCAKUPFFPSGNCNTPGPFQWQ 120
|||||:|||||

Db 116 gtmvtvss 123
||:|||||

QY 121 GTLTVSS 128
||:|||||

RESULT 5

ID R72068 standard; Protein: 98 AA
AC R72068;
DT 26-SEP-1995 (first entry)
DE DP10 VH region.
KW Graves ophthalmopathy associated immunoglobulin protein;
KW orbital antigen; monoclonal antibody; heavy chain; H chain;
KW variable region; autoimmunity.
OS Homo sapiens.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT Region 50..56
FT /label= CDR2
PN WO9508336-A.
PD 30-MAR-1995.
PF 22-SEP-1994; U10756.
PR 22-SEP-1993; US-124469.
PA (NICH-) NICHOLS INST DIAGNOSTICS.
PI McLachlan SM, Papoport B;
DR WPI: 95-139383/18.
DR N-PSDB; Q89327.
PT Graves' ophthalmopathy-associated monoclonal antibody - produced
PT by molecular cloning of immunoglobulin genes by PCR
PS Disclosure; Page 68; 94pp; English.
CC L- and H-chain DNA was amplified by PCR from Graves' orbital
CC tissue and clones encoding autoimmune-associated immunoglobulin
CC fragments were obtained 13/15 clones of H chain (IgG1) genes
CC showed homology to the closest germline genes, DP10 (28q327) and
CC hV1283 (28q328). The DNA (28q329) and corresp amino acid
CC (272270) sequences of the VH region of a representative clone,
CC Q67H1 2, are provided.
SQ Sequence 98 AA;

Query Match 64.2%; Score 524; DR 12; Length 98;
Best Local Similarity 84.8%; Pred. NO. 7.13e-40;
Matches 84; Conservative 10; Mismatches 4; Indels 1; Gaps 1;

Db 1 qqlv-qsgaevkpkpssvkcsksggtfssyalswvrgapqgglewmggiipfgtan 59
|||:|||||

QY 1 EVCLLEQSGAEVKKPSSVKVSKASGGTFSGHVISWVPQAPQGLEWGGSIFFGTGN 60
|||||:|||||

Db 60 yaqkfgrvitadeststymelslsrdsedstavyvcar 98
|||||:|||||

QY 61 SAKKFGFVSVITADESASTAYMELSLRSEDSTAYVYCAK 99
|||||:|||||

RESULT 6

ID W19887 standard; Protein: 123 AA.

AC W19887;
DT 07-DEC-1997 (first entry)
DE CEA-specific antibody CEA6 VH mutant HRA11 sequence.
KW Carcinoembryonic antigen; CEA; human; antibody; scfv;
KW tumour marker; lung cancer; breast cancer; colon cancer;
KW adenocarcinoma; diagnosis.
OS Chimeric Homo sapiens;
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT Region 31..35
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 50..56
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 99..112
FT /label= CDR3
FT /note= "complementarity determining region 3"
PN WO9720932-A1.
PD 12-JUN-1997.

PF 09-DEC-1996; G03043.
PF 11-OCT-1996; GB-021295.
PR 07-DEC-1995; GB-025004.
PR 23-MAY-1996; GB-010824.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

hCEA over soluble hCEA. Preferred (A) include pairings of VH and VI sequences from CEA1-7 (see W19876-85) or their CDR sequences, as well as CEA6 VH and VL variants (see W19886-95) obtained by mutagenesis with chain shuffling. Examples of claimed pairings are IgG1b VH with IgG1b2 or CEA6 VL. (A) is used to detect cells expressing hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.

Sequence 123 AA;

Query Match 64.3%; Score 588; DB 23; Length 123;
Best Local Similarity 71.1%; Pref No 2 31e-39;
Matches 91; Conservative 16; Mismatches 16; Indels 5; Gaps

1 qqqlv--qsgaevkpkgsrvkscagggfnsfpinwlrqapqgglewmgslisfgtan 59
1 EVQLLESGAEVWRPQSSVAVFASGRIFSGHVTSWVPADGCTFEWWSGISSEFGTSN 60

60 yaqfqqgrrltidastetaymcslslrsdcstavvycaqcsnhy--elvyv--ymdvwgg 111
61 SAQKFGQGRVSVITADESASTAYMELSLPSIEDTAIVYCAKPPFPFGSGCTGYPGPFQDQWGQ 120

116 gtmvtvss 123
121 GTLVTVSS 128

Db Db
Qy Qy

RESULT 10
ID R65019 standard; Protein: 147 AA.
AC R65019;
DE 02-OCT-1995 (first entry)
DE 93A9 anti-Varicella zoster virus antibody heavy chain variable region.
DE KW Varicella zoster virus, VZV; anti-VZV monoclonal antibody, 93KA9.
DE KW glycoprotein II subunit; vaccine
DE KW Synthetic.
FH Key Location/Qualifiers
FT Protein 20 147
FT /label= mature light chain
FT Region 50 54
FT /label= complementarity determining region (CDR)
FT Region 69..85
FT /label= CDR
FT Region 118..136
FT /label= CDR
FT /label= FDR
FT WO9504080-A.
PN 09-FEB-1995.
PF 22-JUL-1994; U98241.
PF 28-JUL-1993; US-098479.
PF 24-MAR-1994; US-217918.
PP (SANO) SANDOZ PHARM CORP.
PI Lake P, Ostberg L;
PI WPI; 95-090612/12.
PI N-PSDB; Q82750.
PT Human monoclonal antibodies specific for the glyco:protein II subunit of varicella zoster virus, used in a therapy and prophylaxis of infection
PT Claim 8; Fig 4B; 39pp; English.
PS A human anti-Varicella zoster virus monoclonal antibody was prepd. using the trioma method of Ostberg et al. (1983) Hybridoma 2:361-367.
CC One resultant trioma neutralised VZV in the absence of complement.
CC This cell line, designated cell line TC93KA9, produced an antibody designated 93KA9, cDNA for the light and heavy chain variable region genes of the 93KA9 antibody were cloned using PCR. At least two heavy chain (gamma-1) and two light chain (kappa) specific clones were sequenced (see Q82749 & Q82750 respectively).
CC Sequence 147 AA;

Query Match 63.9%; Score 585; DB 12; Length 147;
Best Local Similarity 70.2%; Pref No. 4 15e-49;
Matches 92; Conservative 15; Mismatches 18; Indels 6; Gaps

20 qqqlv--qsgaevkpkgsrvkscagggfnsfpinwlrqapqgglewmgslisfgtan 111
21 EVQLLESGAEVWRPQSSVAVFASGRIFSGHVTSWVPADGCTFEWWSGISSEFGTSN 120

Db Db
Qy Qy



MPSrch_PP protein - protein database search, using Smith-Waterman algorithm
Pur on: Tue Feb 24 07:04:15 1998; MasPar time 5.78 Seconds
Tabular output not generated.
465,989 Million cell updates/sec
Title: >US-08-844-215-2
Description: (1-127) from US8844215.pep
Perfect Score: 931
Sequence: 1 EVQLLESGAELVKPGSSVKHTMGYFDYWGQGLTVSS 127
Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210398 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 42.278; Variance 75.769; scale 0.558
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	543	58.3	117	5	HV1A_HUMAN IG HEAVY CHAIN V-1 RE	2,650-93
2	491	52.7	117	5	HV1B_HUMAN IG HEAVY CHAIN PRECUP	1,100-81
3	478	51.3	117	5	HV1C_HUMAN IG HEAVY CHAIN PRECUP	8,500-79
4	467	50.2	120	5	HV3C_MOUSE IG HEAVY CHAIN V REGI	2,330-76
5	460	49.4	125	5	HV1E_HUMAN IG HEAVY CHAIN V-1 RE	8,240-75
6	458	49.0	143	5	HV1C_HUMAN IG HEAVY CHAIN PRECUP	2,280-74
7	456	49.0	114	5	HV0C_MOUSE IG HEAVY CHAIN V REGI	6,310-74
8	448	48.1	140	5	HV02_MOUSE IG HEAVY CHAIN PRECUP	3,680-72
9	423	45.4	139	5	HV07_MOUSE IG HEAVY CHAIN PRECUP	1,160-66
10	411	44.1	117	5	HV52_MOUSE IG HEAVY CHAIN PRECUP	4,900-64
11	411	44.1	119	5	HV1D_HUMAN IG HEAVY CHAIN V-1 RE	4,900-64
12	411	44.1	124	5	HV1D_HUMAN IG HEAVY CHAIN V-1 RE	4,900-64
13	409	43.9	138	5	HV48_MOUSE IG HEAVY CHAIN PRECUP	1,340-63
14	408	43.8	117	5	HV04_MOUSE IG HEAVY CHAIN PRECUP	2,220-63
15	404	43.8	117	5	HV06_MOUSE IG HEAVY CHAIN PRECUP	2,220-63
16	408	43.8	122	5	HV3H_HUMAN IG HEAVY CHAIN V-1 RE	2,220-63
17	407	43.7	117	5	HV05_MOUSE IG HEAVY CHAIN PRECUP	3,660-63
18	405	43.5	137	5	HV11_MOUSE IG HEAVY CHAIN PRECUP	1,090-62
19	404	43.4	117	5	HV04_MOUSE IG HEAVY CHAIN PRECUP	1,650-62
20	402	43.2	121	5	HV3J_HUMAN IG HEAVY CHAIN V-1 RE	4,520-62
21	401	43.1	120	5	HV5C_MOUSE IG HEAVY CHAIN V REGI	7,450-62
22	400	43.0	122	5	HV3E_HUMAN IG HEAVY CHAIN V-1 RE	1,170-61

ID	HV1A_HUMAN	STANDARD	PRT	117 AA
AC	P01742			
DT	21-JUL-1986 (REL. 01, CREATED)			
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)			
DT	21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)			
DE	IG HEAVY CHAIN V-1 REGION (EU)			
OS	HOMO SAPIENS (HUMAN)			
CC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
CC	EUTHERIA; PRIMATES			
RN	[1]			
RP	SEQUENCE			
RE	MEDLINE: 71064024			
RA	CUNNINGHAM R.A., RUTISHAUSER N., GALL W.E., GOTTILIER P.D.,			
RA	WAXDAL M.J., EDELMAN G.M.;			
PL	BIOCHEMISTRY 9:3161-3170(1970).			
RN	[2]			
RP	DISULFIDE BOND.			
RE	MEDLINE: 71064027			
RA	GALL W.E., EDELMAN G.M.;			
PL	BIOCHEMISTRY 9:3168-3196(1970).			
CC	-1- THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS MYELOMA PROTEIN HAS			
CC	ALSO BEEN DETERMINED			
DR	PIR: A02023; GIHEU.			
DR	HSP: P01810; 1FVB.			
KW	IMMUNOGLOBULIN V REGION.			
FT	MOTIFS 1			
FT	D-SULFID 22			
FT	NONTER 117			
SC	SEQUENCE 117 AA; 12472 MW; PC99E17D CPC32;			
Query Match	58.3%; Score 543; DB 5; Length 117;			
Best Local Similarity	76.5%; Pred. No. 2,650-93;			
Matches	75; Conservative 11; Mismatches 11; Indels 1; Gaps 1;			
Db	1 qvqlv-gsqavckkpgssvksvskasggtisrsailwrgapqggglwmggipmfgppn 59			
Qy	1 EVQLLESGAELVKPGSSVKVSGVFGDTSPYTIQLPCAPGSGPEWMGNIPTVNTPN 60			
Db	60 yqakfgqrvtidestntatymelsslrdsedatfyca 97			
Qy	61 YAKFGQGLSLTADDSSTAYMELSSLRSEDATVYFCA 98			
RESULT 2	STANDAPE; PRT: 117 AA.			

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AC P01743:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1986 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (HC3)
OS HOMO SAPIENS (HUMAN)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 83144028.
RA RECHAVI G., RAM D., GLAZER L., ZAKUT P., GIVOL D.;
RL PROC. NATL. ACAD. SCI. U.S.A. 80:855-859(1983)
DR EMBL: J00240: G553411; -
DP HSSP: P01810: LFVR
KW IMMUNOGLOBULIN V REGION: SIGNAL
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (HC3)
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 12946 MW: 60084108 CPC32;

Query Match 52.7%; Score 491; DB 5; Length 117;
Best Local Similarity 59.7%; Pred. No. 1,10e-81;
Matches 69; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

Db 20 qvqlv-gsgaevkpgasvkvsckasrtyfnssymhwrqapqgdlwmlngssgs 78
- - - - - ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 EVQLLESGAEVKKPGSSVKSCQVFGDTSRKTIQRLQAPGGPEWMCNIIPVYNTPN 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79 yaqkfqrvttdtststymelsslrssedvayfcar 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 YAQKFGRLSITADSTSTAYMELSSLRSEDVAYFCA 99
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
ID HV1G_HUMAN STANDARD: PRT: 117 AA.
AC P23083:
DT 01-NOV-1991 (REL. 20, CREATED)
DT 01-NOV-1991 (REL. 20, LAST SEQUENCE UPDATE)
DT 01-NOV-1991 (REL. 20, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (V35).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 88296408.
RA MATSUDA F., LEE K.H., NAKAI S., SATO T., KOEIRA M., ZENG S.Q.,
RA OHNO H., FUKUHARA S., HONJO T.;
RL EMBO J. 7:1047-1051(1988).
DR EMBL: X07448: -; NOT_ANNOTATED_CDS.
DR PIR: S00476: HVH035.
DR HSSP: P01810: LFVR.
KW IMMUNOGLOBULIN V REGION: SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (V35)
FT NON_TER 117 117
SQ SEQUENCE 117 AA: 13000 MW: 60056001 CPC32;

Query Match 51.3%; Score 478; DB 5; Length 117;
Best Local Similarity 67.7%; Pred. No. 8.50e-79;
Matches 67; Conservative 11; Mismatches 20; Indels 1; Gaps 1;

Db 20 qvqlv-gsgaevkpgasvkvsckasrtyfnssymhwrqapqgdlwmlngssgs 78
- - - - - ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1 EVQLLESGAEVKKPGSSVKSCQVFGDTSRKTIQRLQAPGGPEWMCNIIPVYNTPN 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 79 yaqkfqrvttdtststymelsslrssedvayfcar 117
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 YAQKFGRLSITADSTSTAYMELSSLRSEDVAYFCA 99
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RESULT 4
ID HV03_MOUSE STANDARD: PRT: 120 AA.
AC P01747:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (46-65).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 8311846.
RA SIEKEVITZ M., GEETEP M.L., RPOUEUR P., RIBLET R.,
RA MARSHAK - POHSTEIN A.;
PL EUP 7: IMMUNOL. 12:1023-1032(1982).
CC -1- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
CC THAT HYBRIDIZE TO THIS ONE. THE AUTHORS CONCLUDE THAT ALL OF
CC THESE V REGIONS HAVE BEEN PLACED TO THE SAME V SEGMENT. H42.
CC
DR PIR: A02024: HVMSG7.
DR HSSP: P01789: 6FAB.
KW IMMUNOGLOBULIN V REGION: ANTIARSONATE ANTIBODY; HYBRIDOMA.
FT NON_TER 120 120
SQ SEQUENCE 120 AA: 13307 MW: 608001 CPC32;

Query Match 50.2%; Score 467; DB 5; Length 120;
Best Local Similarity 56.3%; Pred. No. 2.33e-76;
Matches 71; Conservative 23; Mismatches 23; Indels 6; Gaps 4;

Db 1 vql-rqsgaevkpgasvkvsckasrtyfnssymhwrqapqgdlwmlngssgs 59
- - - - - ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 2 VQLRFGSAEVKKPGSSVKSCQVFGDTSRKTIQRLQAPGGPEWMCNIIPVYNTPN 61
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 nekfkqkttltvdksststymelsslrssedvayfcarvyy---a-syfydywqr 114
- - - - - ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 62 AOKFGRLSITADSTSTAYMELSSLRSEDVAYFCAVVPINAIIRITMGVYFYDYWQRT 121
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 115 lttyss 120
- - - - - |||||
QY 122 LTVSS 127

RESULT 5
ID HV1F_HUMAN STANDARD: PRT: 125 AA.
AC P03226:
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-JAN-1988 (REL. 06, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-I REGION (MOT).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES
RN [1]
RP SEQUENCE.
RX MEDLINE: 86203277.
RA KOJIMA M., KOIDE T., ODANI S., ONO T.;
RL MOL. IMMUNOL. 23:169-174(1986).
DR PIR: A02025: HVH00.
DR HSSP: P01772: 6FAB.
KW IMMUNOGLOBULIN V REGION.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 107 D SEGMENT.
FT MAIN 108 125 D SEGMENT.
FT DISULFID 24 96 BY SIMILARITY.
FT NON_TER 125 125
SQ SEQUENCE 125 AA: 13579 MW: 67450023 CPC32;

Query Match 49.4%; Score 460; DB 5; Length 125;
Best Local Similarity 51.2%; Pred. No. 8.24e-75;
Matches 65; Conservative 25; Mismatches 35; Indels 2; Gaps 2;

Db 1 qvqlv-gsgaevkpgasvkvsckasrtyfnssymhwrqapqgdlwmlngssgs 59
- - - - - ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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QY 1 EVOLLESGAEVKKPGSSVAVSCQVFGDTFSPYTIQWLRCAPGCGPFWGNIPVYNTPN 60
Db 60 ygprsqarfvtvtdstttvymeltalisdaiyycarga-hysdtdsdgtslpgwgg 118
QY 61 YAKFOGFLSITADOSTSTAYMELSSIPSRDTAVYFCAPVVPNAIPHTMGVYFDVWGCG 120
Db 119 tltvss 125
QY 121 TLTVSS 127

RESULT 6
ID HVIC_HUMAN STANDARD: PPT: 143 AA
AC P01744:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V-I REGION (ND) (FRAGMENTS).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
PN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83065234.
FA KENTEN J H, MORGAPARD H V, HUGHTON M., DEFRYSHE P B., VINEY J,
FA RELL L O., GOULD H J.
RL PROC. NATL. ACAD. SCI. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 16-142.
FA RENNICH H H., JOHANSSON S G.O., VON RAHR-LINDSTROM H.;
RL (IN) IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS,
RL BACH M.K., ED., PP.1-36, MARCEL DEKKER, NEW YORK, (1978).
CC -I- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A02026; EIHUND.
DR HSSP: P01607; IFGV.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT NON_CONS 4 5
FT SIGNAL 1 15
FT CHAIN 16 143 IG HEAVY CHAIN V REGION (ND).
FT MOD_RES 16 16 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 37 111
FT CONFLICT 17 17 T -> V (IN REF. 2).
FT CONFLICT 49 50 IH -> HI (IN REF. 2).
FT CONFLICT 63 64 VG -> GV (IN REF. 2).
FT CONFLICT 121 121 MISSING (IN REF. 2).
FT NON_TER 143 143
SQ SEQUENCE 143 AA; 16051 MW; 6D605E13 CRC32;

Query Match 49.28; Score 458; DB 5; Length 143;
Best Local Similarity 53.8%; Pred. No. 2,28e-74;
Matches 70; Conservative 24; Mismatches 31; Indels 5; Gaps 5,

Db 16 qtlv-qsgaevkpgssvavscqvfgdtf-srytiqlwlrqapggpewgnliPVYNTP 73
QY 1 EVOLLESGAEVKKPGSSVAVSCQVFGDTF-SRYTIQLWLRQAPGCGPFWGNIPVYNTP 59
Db 74 nyaprfgrvtrtdasfstaymdrlsrdsdsvayfcskdpfwsdyvndfytyldvw 133
QY 60 NYAOKFOGRLSITADOSTSTAYMELSSIPSRDTAVYFCAPV-VI-PNAIPHTMGVYFDVW 117
Db 134 qggtvtvss 143
QY 118 GQGLTLTVSS 127

RESULT 7
ID HV00_MOUSE STANDARD: PPT: 114 AA.
AC P01741:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
OS MUS MUSCULUS (MOUSE).

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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
RX STRAIN-A/J;
RX MEDLINE; 79195438.
RA CAPRA J.D., NISONOFF A.;
RA J. IMMUNOL. 123:279-284(1979).
CC -I- ANTIBODY ISOLATED FROM TEN MTCE WAS EXCLUSIVELY OF THE IGG1
CC SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V REGION
CC SEQUENCE.
DR PIR: A02022; GIMSA.
DR HSSP: P01772; IFGV.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 1A027FID CRC32;

Query Match 49.0%; Score 456; DB 5; Length 114;
Best Local Similarity 69.6%; Pred No 6.31e-74;
Matches 71; Conservative 13; Mismatches 16; Indels 2; Gaps 2;

Db 1 evql-qsgaevlkagssvkmkskatsytfsscylywrgapagglcdlyssssaypn 59
QY 1 EVOLLESGAEVKKPGSSVAVSCQVFGDTFISRYTIQLWLRQAPGCGPFWGNIPVYNTPN 60
Db 60 yaqkfgrvtitadostntaymelsslrscdtavvfcavri 101
QY 61 YAKFOGRLSITADOSTSTAYMELSSLRSDTAVYFCA-RVV 101

RESULT 8
ID HV02_MOUSE STANDARD: PPT: 140 AA.
AC P01746:
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-A/J;
RX MEDLINE; 82152818.
RA S.M.S.J., FABBRI T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
RA CAPRA J.D.;
RA SCIENCE 216:309-311(1982).
DR EMBL; J00493; G195007; -.
DR PIR: A02028; HVM5G7.
DR HSSP: P01789; 6FAB.
KW IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY; HYPERICAMA; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION (93G7).
FT NON_TER 140 140
SQ SEQUENCE 140 AA; 15514 MW; 0700D5C8 CRC32;

Query Match 48.1%; Score 448; DB 5; Length 140;
Best Local Similarity 55.9%; Pred. No. 3.68e-72;
Matches 71; Conservative 20; Mismatches 30; Indels 6; Gaps 4;

Db 20 evql-qsgaevlragssvkmkskatsytfssyginvkvprgpgglewiyigpggyin 78
QY 1 EVOLLESGAEVKKPGSSVAVSCQVFGDTFISRYTIQLWLRQAPGCGPFWGNIPVYNTPN 60
Db 79 ynefkqkttltvdksststamqlrsltsodsavvfcar---sh---ygggydfdwgg 133
QY 61 YAKFOGRLSITADOSTSTAYMELSSLRSDTAVYFCARVVIAPHTMGVYFDVWGCG 120
Db 134 tpltvss 140
QY 121 TLTVSS 127

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RESULT 9
ID HV07_MOUSE STANDARD; PRT: 139 AA.
AC P01751; P01752;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-JUL-1986 (REL. 34, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (H1-8 / 186-2)
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6;
RX MEDLINE; 81234546.
PA ROTHWELL A L M, PASKIND M, RETH M, IMANISHI-KAPI T, RAJEWSKY K.,
RA BALTIMORE D.;
PL CELL 24:525-637(1991)
CC -1- THE B1-8 MG CHAIN MPNA WAS CLONED FROM A HYBRIDOMA MAKING
CC ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL (NPB
CC ANTIBODIES).
DR EMBL; J00529; G195115;
DR PIR; AC2034; MMS18.
DR HSP; P01810; 1UHL.
KW IMMUNOGLOBULIN V REGION; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 139 IG HEAVY CHAIN V REGION (H1-8 / 186-2).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 139 139
SQ SEQUENCE 139 AA; 15410 MW; DEB2C7DA CPC32;

Query Match 45.4%; Score 423; DB 5; Length 139;
Best Local Similarity 51.2%; Pred. No. 1,600-66;
Matches 65; Conservative 27; Mismatches 28; Indels 7; Gaps 6;

Db 20 qvql qggqavkppqalvskskasytftsydinwkwkqppqqlwkwlypqqstsk 79
QY 1 FVQILESGAPVKKPGSSVKVSCVFGTFTSFYTIQWLKQAPQGSGPEWMNIPVYNIPN 60
Db 79 ynefkkskaltvdksptstymqlssltssdsayyyfcar--y--d--y--yssy--fd--wggg 132
QY 61 YAKRFQGLSITADGSTSTAYMEUSSLPSEDTAVYFAPVVPVNPATPHMGVYFVWGG 120
Db 133 tlttvss 139
QY 121 TLTIVSS 127

RESULT 10
ID HV52_MOUSE STANDARD; PRT: 117 AA.
AC P06327;
DT 01-JAN-1988 (REL. 06, CREATED)
DT 01-JAN-1988 (REL. 06, LAST SEQUENCE UPDATE)
DT 01-NOV-1990 (REL. 16, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN PRECURSOR V REGION (VH58 AL/A4).
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85099340.
PA YANCOPOULOS G.D., ALT F.W.;
PL CELL 40:271-281(1985);
DR EMBL; M13787; G466291;
DR PIR; A02029; HVMSA1.
DR HSP; P01772; 1FVOR.
KW IMMUNOGLOBULIN V REGION; SIGNAL.

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FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (VH58 AL/A4).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; A50F2B13 CPC32;

Query Match 44.1%; Score 411; DB 5; Length 117;
Best Local Similarity 56.6%; Pred. No. 4,900-64;
Matches 56; Conservative 20; Mismatches 22; Indels 1; Gaps 1;

Db 20 qvql qggqavkppqalvskskasytftsydinwkwkqppqqlwkwlypqqstsk 79
QY 1 EVQLLESGSFAEVKPKSSVKVSCVFGTFTSFYTIQWLKQAPQGSGPEWMNIPVYNIPN 60
Db 79 ynefkkskaltvdksptstymqlssltssdsayyyfcar 117
QY 61 YAKRFQGLSITADGSTSTAYMEUSSLPSEDTAVYFAP 99

RESULT 11
ID HV31_HUMAN STANDARD; PRT: 119 AA.
AC P01770;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-III REGION (NIF).
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE
RX MEDLINE; 77070269.
PA PONTING L H., HILSCHMANN N.;
PA HOPPE-SEYLER S 2, PHYSIOL. CHEM 357:1571-1604(1976).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE; 77070267.
PA DPEKEP L., SCHWAB J., REICHEL W., HILSCHMANN N.;
PA HOPPE-SEYLER S 2, PHYSIOL. CHEM 357:1515-1540(1976).
CC -1- THIS CHAIN WAS ISOLATED FROM AN 1991 MYELOMA PROTEIN.
DR PIR; A02053; GHUNI.
DR HSP; P01607; 1FQV.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 13242 MW; 5703CABE CPC32;

Query Match 44.1%; Score 411; DB 5; Length 119;
Best Local Similarity 50.0%; Pred. No. 4,900-64;
Matches 64; Conservative 31; Mismatches 23; Indels 10; Gaps 6;

Db 1 qvqlv-qsgqavvqpsrlrlscaasntftsrlylhvrdapvklwvva-vmsylpbbk 58
QY 1 EVQLLESGSFAEVKPKSSVKVSCVFGTFTSFYTIQWLKQAPQGSGPEWMNIPVYNIPN 60
Db 59 hyadsvgrftsrlnsktlylhmnsllrpdtaavyyfcar--trdt---am---flahwq 111
QY 60 NVACKFQGLSITADGSTSTAYMEUSSLPSEDTAVYFAPVVPVNPATPHMGVYFVWGG 119
Db 112 gtlvtvss 119
QY 120 GTIVTVSS 127

RESULT 12
ID HV1D_HUMAN STANDARD; PRT: 124 AA.
AC P01760;

```



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FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION (102).
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON-TER 117 117
SQ SEQUENCE 117 AA: 12867 MW: 48001982 CRC32:

Query Match 43.8%; Score 408; DB 5; Length 117;
Best Local Similarity 58.8%; Pred. No. 2.22e-63;
Matches 57; Conservative 18; Mismatches 21; Indels 1; Gaps 1;

Db 21 vql-qgpgaelvkpgasvkvsckasqyftfyswmhvwkqpgqglewigrhbpsdsdtny 79
QY 2 VQLLEGSGAEVKPGSSVKVSCQVFGDTFSRYTIQWLKQAPQGGPPWMMGNIIIPVYNTPNY 61

Db 80 nskfkakatltdkssstaymqllssitsedsavyyca 116
QY 62 AQRFGRLSITADDSTSTAYMELSLURSEDATVYFCA 98

```

Search completed: Tue Feb 24 07:04:39 1998
Job time : 24 secs.

M P E R E H

(TM)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:04:59 1998: MspPar time 8.21 Seconds
471.531 Million cell updates/sec
Tabular output not generated.

Title: >US-08-844-215-2
Description: (-127) from US08844215 pep
Perfect Score: 931
Sequence: 1 EVQLLEQSGAEVKKPQSSVKHTMGYFDYWGQGLTVSS 127

Scoring table: PAM 150
Gap 11

Searched: 95051 seqs, 30469580 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: pir53
1:ann1 2:ann2 3:ann3 4:ann4 5:annn1 6:annn2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann11 16:unann12 17:unann
18:unrev

Statistics: Mean 41.781; Variance 118.597; scale 0.352

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description	Pred No.
1	658	70.7	126	7 B33548	Ig heavy chain V-1 r 1.46e-74	
2	658	70.7	127	7 PH0955	Ig heavy chain V-1 r 1.46e-74	
3	631	67.8	129	7 A33548	Ig heavy chain V-1 r 1.11e-70	
4	625	67.1	125	7 PH0957	Ig heavy chain V-1 r 8.08e-70	
5	624	67.0	120	7 PH0962	Ig heavy chain V-1 r 1.12e-69	
6	622	66.8	123	7 PH0958	Ig heavy chain V-1 r 2.18e-69	
7	613	65.8	128	7 PH0952	Ig heavy chain V-1 r 4.25e-68	
8	605	65.0	132	7 S46394	Ig heavy chain V-1 r 5.95e-67	
9	604	64.9	133	7 C33548	Ig heavy chain V-1 r 8.27e-67	
10	504	54.9	527	7 S24683	Ig mu chain precurs 8.27e-67	
11	603	64.8	123	7 S44108	Ig heavy chain V-D-J 1.15e-66	
12	599	64.3	132	7 PH0954	Ig heavy chain V-1 r 4.30e-66	
13	596	64.0	122	7 B49590	Ig heavy chain V-1 r 1.15e-65	
14	586	62.9	119	7 S44106	Ig heavy chain V-D-J 3.11e-64	
15	578	62.1	135	7 S36351	Ig heavy chain V-1 r 4.31e-63	
16	578	62.1	136	7 PH0960	Ig heavy chain V-1 r 4.31e-63	
17	572	61.4	98	7 S26915	Ig heavy chain V-1 r 3.10e-62	
18	572	61.4	116	7 PH0959	Ig heavy chain V-1 r 3.10e-62	
19	572	61.4	116	7 S31598	Ig heavy chain V-1 r 3.10e-62	
20	572	61.4	119	7 PH0961	Ig heavy chain V-1 r 3.10e-62	

21	572	61.4	135	7 PH0953	Ig heavy chain V-1 r 3.10e-62
22	572	61.4	142	7 A32483	Ig heavy chain V-1 r 3.10e-62
23	570	61.2	98	7 S24680	Ig heavy chain V-1 r 2.97e-62
24	570	61.2	121	7 A49590	Ig heavy chain V-1 r 3.08e-61
25	565	60.7	124	7 S19565	Ig heavy chain V-1 r 5.94e-61
26	563	60.5	122	7 C49590	Ig heavy chain V-1 r 4.25e-60
27	557	59.8	113	7 PH1563	Ig heavy chain V-1 r 1.58e-59
28	553	59.4	98	7 S46463	Ig heavy chain V-1 r 5.84e-59
29	549	59.0	122	7 S36371	Ig heavy chain V-1 r 2.16e-58
30	545	58.5	123	7 D33548	Ig heavy chain V-1 r 4.16e-58
31	543	58.3	117	2 G1H0EU	Ig heavy chain V-1 r 5.78e-58
32	542	58.2	97	7 PH0870	Ig heavy chain V-1 r 1.54e-57
33	539	57.9	127	7 S34014	Ig heavy chain V-1 r 4.11e-57
34	539	57.9	135	7 B32374	Ig heavy chain V-1 r 7.90e-57
35	536	57.6	136	7 PH0536	Ig heavy chain V-1 r 4.04e-56
36	534	57.4	116	7 S31867	Ig heavy chain V-1 r 7.77e-56
37	529	56.8	118	7 PH1866	Ig heavy chain V-1 r 2.08e-55
38	527	56.6	98	7 A30523	Ig heavy chain V-1 r 1.49e-55
39	526	56.5	129	7 S36360	Ig heavy chain V-1 r 1.06e-54
40	525	56.4	118	7 S36365	Ig heavy chain V-1 r 1.46e-54
41	519	55.7	109	7 PH1671	Ig heavy chain V-1 r 2.03e-54
42	518	55.6	108	7 PH1564	Ig heavy chain V-1 r 2.03e-54
43	517	55.5	114	7 PH1867	Ig heavy chain V-1 r 2.03e-54
44	517	55.5	148	7 S29257	Ig heavy chain V-1 r 2.03e-54
45	517	55.5	160	7 F20105	anti-PP2 erythrocyte 2.03e-54

ALIGNMENTS

RESULT 1
ENTRY Ig heavy chain V-1 region (AND) - human
TITLE #formal_name Homo sapiens #common_name man
ORGANISM 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
DATE 16-Aug-1996
ACCESSIONS B33548
REFERENCE A33548
#authors Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, F.P.; Carson, D.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
#cross-references MUID:89345575
#accession B33548
#status preliminary; nucleic acid sequence not shown; not compared with conceptual translation
#molecule_type DNA
#residues 1-126 #label KIP
#experimental_source the sequence was determined from the differentiated gene

CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE #domain immunoglobulin homology #label IMM
15-38 #length 126 #molecular-weight 13710 #checksum 4068
SUMMARY

Query Match 70.7%; Score 658; DB 7; Length 126;
Best Local Similarity 73.2%; Pred. No. 1.46e-74;
Matches 93; Conservative 13; Mismatches 20; Indels 1; Gaps 1;
Db 1 qvqlv-qsgaevkpkssvkvskaggtfssyaiswvrgpqqglwngliifgtan 59
QY 1 EVQLLEQSGAEVKKPQSSVKVSQVFDTSRFTIQLKQAPQGPEWGNIIPTVNTEN 60
Db 50 yadqfgrvritadeststaymolsslrdsdtavycarvsifgvqghyryymdwglg 119
QY 61 YAKRFQGLSLTADSTAYMELSLRSETAVYFCARVVPFAIKHTMGYFDYWGQ 120
Db 120 tvtvss 126
QY 121 TLTVSS 127

```

2
RESULT 2
ENTRY PH0955 #type fragment
TITLE Ig heavy chain V region (G6+ CLL-AND) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0955
REFERENCE #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies
#cross-references MUID:92202880
#accession PH0955
##status nucleic acid sequence not shown
##molecule_type DNA
##residues 1-127 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 1-30
15-98 #region framework 1\
31-35 #domain immunoglobulin homology #label IMM\
36-50 #region complementarity-determining 1\
51-67 #region framework 2\
58-98 #region complementarity-determining 2\
99-115 #region framework 3\
99-115 #region complementarity-determining 3
SUMMARY #length 127 #checksum 5297

Query Match 70.7% Score 658; DB 7; Length 127;
Best Local Similarity 72.7% Pred No 1 46e-74;
Matches 93; Conservative 14; Mismatches 19; Indels 2; Gaps 2;

Db 1 qvqlv-qsgaevkpkssvkvskasggtfssyaiswrrqapqqlwmgqilpiftan 59
QY 1 EVQLLEGGSGAEVKKPGSSVKVSQCQVFDTSPYTLTWLPGAPGQSPWMGNIPVYNTN 60
Db 60 yaqkfgrvritadeststymelsslrsestavyycarvsiqvvqhyvyyvyyvdywk 119
QY 61 YAQKFGQPLSLTADDSSTAYMELSSLRSEDTAVYFCAPVTPNAPHTMGYFFDYWQ 119
Db 120 gttvtvss 127
QY 120 GTLVTVSS 127

Query Match 70.7% Score 658; DB 7; Length 127;
Best Local Similarity 72.7% Pred No 1 46e-74;
Matches 93; Conservative 14; Mismatches 19; Indels 2; Gaps 2;

RESULT 3
ENTRY A33548 #type complete
TITLE Ig heavy chain V-1 region (NE1) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996
ACCESSIONS A33548; PH0955
REFERENCE #authors Kipps, T.J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.; Carson, D.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin heavy chain variable region gene expressed at high frequency in chronic lymphocytic leukemia.
#cross-references MUID:89345575
#accession A33548
##status preliminary: not compared with conceptual translation
##molecule_type mRNA
##residues 1-120 ##label KIP
REFERENCE PH0952
#authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies
#cross-references MUID:92202880
#accession PH0955
##status nucleic acid sequence not shown
##molecule_type DNA

```

```

##residues 1-129 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 1-30
15-98 #region framework 1\
31-35 #domain immunoglobulin homology #label IMM\
36-50 #region complementarity-determining 1\
51-67 #region framework 2\
58-98 #region complementarity-determining 2\
99-117 #region framework 3\
99-117 #region complementarity-determining 3
SUMMARY #length 129 #molecular_weight 13932 #checksum 4075

Query Match 67.8% Score 631; DB 7; Length 129;
Best Local Similarity 70.8% Pred. No 1.11e-70;
Matches 92; Conservative 17; Mismatches 17; Indels 4; Gaps 3;

Db 1 qvqlv-qsgaevkpkssvkvskasggtfssyaiswrrqapqqlwmgqilpiftan 59
QY 1 EVQLLEGGSGAEVKKPGSSVKVSQCQVFDTSPYTLTWLPGAPGQSPWMGNIPVYNTN 60
Db 60 yaqkfgrvritadeststymelsslrsestavyycarvsiqvvqhyvyyvyyvdywk 119
QY 61 YAQKFGQPLSLTADDSSTAYMELSSLRSEDTAVYFCARV-VTPNAL-RHIMGYVFDW 117
Db 120 ggttlvtvss 129
QY 118 GCGTLVTVSS 127

RESULT 4
ENTRY PH0957 #type fragment
TITLE Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0957
REFERENCE #authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:42201880
#accession PH0957
##status nucleic acid sequence not shown
##molecule_type DNA
##residues 1-125 ##label MAR
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE 1-30
15-98 #region framework 1\
31-35 #domain immunoglobulin homology #label IMM\
36-50 #region complementarity-determining 1\
51-67 #region framework 2\
58-98 #region complementarity-determining 2\
99-113 #region framework 3\
99-113 #region complementarity-determining 3
SUMMARY #length 125 #checksum 8143

Query Match 67.1% Score 625; DB 7; Length 125;
Best Local Similarity 71.7% Pred No 9.08e-70;
Matches 91; Conservative 14; Mismatches 20; Indels 2; Gaps 2;

Db 1 qvqlv-qsgaevkpkssvkvskasggtfssyaiswrrqapqqlwmgqilpiftan 59
QY 1 EVQLLEGGSGAEVKKPGSSVKVSQCQVFDTSPYTLTWLPGAPGQSPWMGNIPVYNTN 60
Db 60 yaqkfgrvritadeststymelsslrsestavyycarvsiqvvqhyvyyvyyvdywk 118
QY 61 YAQKFGQPLSLTADDSSTAYMELSSLRSEDTAVYFCARVTPNAPHTMGYVFDW 126
Db 119 tlvtvss 125
QY 121 TLTVTVSS 127

```

```

SUMMARY          #length 122  #checksum 7292

Query Match      65.8%; Score 622; DB 7; Length 122;
Best Local Similarity 73.2%; Pred No 2.18e-68;
Matches 93; Conservative 15; Mismatches 14; Indels 5; Gaps 3;

Db 1  qvqlv-qsgaevkpkgsyvkscasggtfssyalswvrgagqglewmgiipifctan 59
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1  EVQLLEQSGAEVKKPKSSVKVSCQVFGDTFSPYTIQLKPAQCQCPEWMGNIPVYNTPN 60
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 60  yaqkfgrvritadestaymelsslrdsatavyyarv--fpplffavg--d-wggg 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61  YAKKFGKSLTADNSTAYMELSSLPSEDTAVYFAPVVPNAIPHTMGYFDFWGGG 120
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 116  tlvtvss 122
      |||||
Qy 121  TLVTVSS 127
      |||||

RESULT 7
ENTRY   PH0952      #type fragment
TITLE   Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE    17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
        16-Aug-1996
ACCESSIONS PH0952
REFERENCE   Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
            J. Exp. Med. (1992) 175:983-991
            Evidence for somatic selection of natural autoantibodies
            #cross-references MUID:92202880
            #accession PH0952
            #status nucleic acid sequence not shown
            #molecule_type DNA
            #residues 1-122 #label MAP
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30      #region framework 1\
15-98     #domain immunoglobulin homology #label IMM\
31-35     #region complementarity-determining 1\
36-50     #region framework 2\
51-67     #region complementarity-determining 2\
68-98     #region framework 3\
99-108    #region complementarity-determining 3
SUMMARY   #length 120  #checksum 5559

Query Match      73.0%; Score 624; DB 7; Length 120.
Best Local Similarity 73.2%; Pred No 1.12e-69;
Matches 93; Conservative 14; Mismatches 13; Indels 7; Gaps 5;

Db 1  qvqlv-qsgaevkpkgsyvkscasggtfssyalswvrgagqglewmgiipifctan 59
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1  EVQLLEQSGAEVKKPKSSVKVSCQVFGDTFSPYTIQLKPAQCQCPEWMGNIPVYNTPN 60
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 60  yaqkfgrvritadestaymelsslrdsatavyyarvga-g-r-p---hfdywgqg 113
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61  YAKKFGKSLTADNSTAYMELSSLPSEDTAVYFAPVVPNAIPHTMGYFDFWGGG 120
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 114  tlvtvss 120
      |||||
Qy 121  TLVTVSS 127
      |||||

RESULT 6
ENTRY   PH0958      #type fragment
TITLE   Ig heavy chain V region (G6+ CLL-HUR) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE    17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
        16-Aug-1996
ACCESSIONS PH0958
REFERENCE   Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
            J. Exp. Med. (1992) 175:983-991
            Evidence for somatic selection of natural autoantibodies
            #cross-references MUID:92202880
            #accession PH0958
            #status nucleic acid sequence not shown
            #molecule_type DNA
            #residues 1-122 #label MAP
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30      #region framework 1\
15-98     #domain immunoglobulin homology #label IMM\
31-35     #region complementarity-determining 1\
36-50     #region framework 2\
51-67     #region complementarity-determining 2\
68-98     #region framework 3\
99-110    #region complementarity-determining 3

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SUMMARY          #length 122  #checksum 7292

Query Match      65.8%; Score 622; DB 7; Length 122;
Best Local Similarity 73.2%; Pred No 2.18e-68;
Matches 93; Conservative 15; Mismatches 14; Indels 5; Gaps 3;

Db 1  qvqlv-qsgaevkpkgsyvkscasggtfssyalswvrgagqglewmgiipifctan 59
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1  EVQLLEQSGAEVKKPKSSVKVSCQVFGDTFSPYTIQLKPAQCQCPEWMGNIPVYNTPN 60
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 60  yaqkfgrvritadestaymelsslrdsatavyyarv--fpplffavg--d-wggg 115
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61  YAKKFGKSLTADNSTAYMELSSLPSEDTAVYFAPVVPNAIPHTMGYFDFWGGG 120
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 116  tlvtvss 122
      |||||
Qy 121  TLVTVSS 127
      |||||

RESULT 7
ENTRY   PH0952      #type fragment
TITLE   Ig heavy chain V region (G6+ CLL-SMI) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE    17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
        16-Aug-1996
ACCESSIONS PH0952
REFERENCE   Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
            J. Exp. Med. (1992) 175:983-991
            Evidence for somatic selection of natural autoantibodies.
            #cross-references MUID:92202880
            #accession PH0952
            #status nucleic acid sequence not shown
            #molecule_type DNA
            #residues 1-128 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region: immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30      #region framework 1\
15-98     #domain immunoglobulin homology #label IMM\
31-35     #region complementarity-determining 1\
36-50     #region framework 2\
51-67     #region complementarity-determining 2\
68-98     #region framework 3\
99-116    #region complementarity-determining 3
SUMMARY   #length 128  #checksum 3537

Query Match      65.8%; Score 613; DB 7; Length 128;
Best Local Similarity 70.5%; Pred No 4.25e-68;
Matches 91; Conservative 15; Mismatches 20; Indels 3; Gaps 3;

Db 1  qvqlv-qsgaevkpkgsyvkscasggtfssyalswvrgagqglewmgiipifctan 59
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 1  EVQLLEQSGAEVKKPKSSVKVSCQVFGDTFSPYTIQLKPAQCQCPEWMGNIPVYNTPN 60
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 60  yaqkfgrvritadestaymelsslrdsatavyyarvga-g-r-p---hfdywgqg 119
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 61  YAKKFGKSLTADNSTAYMELSSLPSEDTAVYFAPVVPNAIPHTMGYFDFWGG 118
      ::::: ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 120  qdtmvtvss 128
      |||||
Qy 119  QDTMVTVSS 127
      |||||

RESULT 8
ENTRY   S46394      #type complete
TITLE   Ig heavy chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE    27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
        23-May-1997
ACCESSIONS S46394
REFERENCE   Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.

```

```

#journal J. Mol. Biol. (1994) 239:68-78
#title In vitro assembly of repertoires of antibody chains on the
#       surface of phage by renaturation.
#accession S46394
##status preliminary
##molecule_type DNA
##residues 1-132 ##label FIG
##cross-references EMBL:Z31681
CLASSIFICATION #superfamily immunoglobulin V region, immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 132 #molecular-weight 14293 #checksum 7515

Query Match 65.0%; Score 605; DB 7; Length 132;
Best Local Similarity 68.4%; Pred. No. 5,95e-67;
Matches 91; Conservative 18; Mismatches 17; Indels 7; Gaps 5;

Db 1 qvqlv-qsgaevkpgssvkvscasqgtfssyaiswvrqpggglewmqgllpifgtan 59
QY 1 EVQLLEQSGAEVKPKGSSVKVSCQVFGDTFSPTTIQWLFPQAPGQGPENWGNIIPVYNTPN 60
Db 60 haqkfgrvritadeststamelsrlsedtavycaktgllqysgswypnsdyvyyg 119
QY 61 YAAKFQGRISITADDTSTAYMELSLRSEDYAVYFCARV--NA-IRHTMG--YYF- 114
Db 120 mdwvqggtttvss 132
QY 115 DYWGQGTILTVSS 127

RESULT 9
ENTRY C33548 #type complete
TITLE Ig heavy chain V-1 region (783) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996
ACCESSIONS C33548
REFERENCE #authors
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin heavy chain
#       variable region gene expressed at high frequency in chronic
#       lymphocytic leukemia.
#cross-references MUID:89345575
#accession C33548
##status preliminary; nucleic acid sequence not shown; not
#       compared with conceptual translation
##molecule_type DNA
##residues 1-133 ##label KIP
##experimental_source the sequence was determined from the
#       differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 133 #molecular-weight 14350 #checksum 1289

Query Match 64.9%; Score 604; DB 7; Length 133;
Best Local Similarity 67.9%; Pred. No. 8,27e-67;
Matches 91; Conservative 19; Mismatches 16; Indels 8; Gaps 6;

Db 1 qvqlv-qsgaevkpgssvkvscasqgtfssyaiswvrqpggglewmqgllpifgtan 59
QY 1 EVQLLEQSGAEVKPKGSSVKVSCQVFGDTFSPTTIQWLFPQAPGQGPENWGNIIPVYNTPN 60
Db 60 haqkfgrvritadeststamelsrlsedtavycaktgllqysgswypnsdyvyyg 119
QY 61 YAAKFQGRISITADDTSTAYMELSLRSEDYAVYFCARV--VI-P-NAIRHTMG--YYF- 114
Db 120 mdwvqggtttvss 133
QY 115 DYWGQGTILTVSS 127

```

QY 115 -DYWGQGTILTVSS 127

RESULT 10

```

ENTRY S14683 #type complete
TITLE Ig mu chain precursor, membrane-bound (clone 201) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
16-Aug-1996
ACCESSIONS S14683
REFERENCE #authors
#journal Nucleic Acids Res. (1990) 18:4278
#title Complete nucleotide sequence of the membrane form of the
#       human IgM heavy chain.
#cross-references MUID:90332450
#accession S14683
##molecule_type mRNA
##residues 1-627 ##label FRI
##cross-references EMBL:X17115
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS immunoglobulin; membrane protein
FEATURE
1-15 #domain signal sequence #status predicted #label SIG
16-627 #product Ig mu chain #status predicted #label MATN
34-117 #domain immunoglobulin homology #label IMM
SUMMARY #length 627 #molecular-weight 68510 #checksum 8581

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Query Match 64.9%; Score 604; DB 7; Length 627;

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Best Local Similarity 67.9%; Pred. No. 8,27e-67;
Matches 91; Conservative 19; Mismatches 16; Indels 8; Gaps 6;

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Db 20 qvqlv-qsgaevkpgssvkvscasqgtfssyaiswvrqpggglewmqgllpifgtan 78

```

QY 1 EVQLLEQSGAEVKPKGSSVKVSCQVFGDTFSPTTIQWLFPQAPGQGPENWGNIIPVYNTPN 60

```

Db 79 yaqkfgrvritadeststamelsrlsedtavycaktgllqysgswypnsdyvyyg 118

```

QY 61 YAAKFQGRISITADDTSTAYMELSLRSEDYAVYFCARV--VI-P-NAIRHTMG--YYF- 114

```

Db 139 mdwvqggtttvss 152

QY 115 -DYWGQGTILTVSS 127

RESULT 11

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ENTRY S44108 #type complete
TITLE Ig heavy chain V-D-J region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change
23-May-1997
ACCESSIONS S44108
REFERENCE #authors
#submission submitted to the EMBL Data Library, March 1994
#description idiotypic vaccination against human B-cell lymphoma: rescue
#       of variable region gene sequences from biopsy material for
#       assembly as single chain iv "personal" vaccine.
#accession S44108
##status preliminary
##molecule_type DNA
##residues 1-123 ##label HAW
##cross-references EMBL:Z31397
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY #domain immunoglobulin homology #label IMM
#length 123 #molecular-weight 13307 #checksum 1747

```

Query Match 64.8%; Score 603; DB 7; Length 123;

```

Best Local Similarity 69.8%; Pred. No. 1,15e-66;
Matches 81; Conservative 17; Mismatches 16; Indels 2; Gaps 2;

```



```

REFERENCE      S36256
#authors      Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.;
               Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
               Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
               G.
#journal      EMBO J. (1993) 12:725-734
#title       Human anti-self antibodies with high specificity from phage
               display libraries.
#accession    S36261
#status      preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues     1-116 #label GRI
#cross-references EMBL:Z18841
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS       heterotetramer; immunoglobulin
FEATURE        15-98
SUMMARY        #domain immunoglobulin homology #label IMM
               #length 116 #checksum 7971

Query Match      62.18; Score 578; DB 7; Length 116;
Best Local Similarity 69.58; Pred. No. 4.31e-63;
Matches 82; Conservative 14; Mismatches 19; Indels 3; Gaps 3;

Db      1 qvql-qesgaevkpgssvkvsckasgdtfssvaiswvrgapggglewmgiipifgtan 59
        . . . . .
QY      1 EVQLLEQSGAEVKKPGSSVKVSQVFGDTFSRYTIQWLRAQPGGPEWMGNIIIPVYNTFN 60
        . . . . .

Db      60 yaqkfgrvtadeststaymelsslrsestavyycargplr-gydyvy-yymdwvg 115
        . . . . .
QY      61 YAAKFOGRLSITADDSTSTAYMEISSURSEDATVYFCARVVIPIAHTMGYYFDYWG 118
        . . . . .

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Search completed: Tue Feb 24 07:05:34 1998
 Job time : 35 secs.

WIRE

(TW)

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on Tue Feb 24 07:33:22 1998. MaxPar time 3.39 Seconds
Tabular output not generated. 190,958 Million cell updates/sec

Title: >US-08-844-215-2
Description: (1-127) from US08844215.pep
Perfect Score: 931
Sequence: 1 EVQLLEQSGAEVKKPGSSVK HTMGYPDYWGCTLTIVSS 127

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs. 5095871 residues

Post-processing: Minimum Match 0*
Lasting first 45 summaries

Database: a-issued
1.back1 2.51 3.52 4.53 5.54 6.55 7.56 8.57 9.58 10.59
10.pct92 11.pct93 12.pct94 13.pct95 14.pct96

Statistics: Mean 26.297 Variance 150.259 Scale 0.180

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	616	66.2	147	US-08-217-918-4	Sequence 4, Application	5,456-39
2	603	64.7	120	PCT-US95-0	Sequence 12, Applicati	6,858-38
3	583	62.6	129	PCT-US95-0	Sequence 45, Applicati	2,138-36
4	579	62.2	120	PCT-US93-1	Sequence 13, Applicati	4,406-46
5	565	60.7	122	PCT-US95-0	Sequence 2, Applicatio	5,538-35
6	551	59.2	128	US-08-478-	Sequence 63, Applicati	6,938-34
7	550	59.1	103	PCT-US92-1	Sequence 63, Applicati	9,308-34
8	550	59.1	102	US-08-053-	Sequence 63, Applicati	8,308-34
9	550	59.1	102	PCT-US92-0	Sequence 55, Applicati	8,308-34
10	550	59.1	102	US-07-834-	Sequence 55, Applicati	8,308-34
11	548	58.9	140	PCT-US93-1	Sequence 12, Applicati	1,198-33
12	545	58.6	121	US-08-354-	Sequence 3, Applicatio	1,716-33
13	545	58.5	121	PCT-US93-1	Sequence 8, Applicatio	2,058-33
14	543	58.3	117	US-08-477-	Sequence 104, Applicati	2,928-33
15	543	58.3	117	US-08-487-	Sequence 72, Applicati	2,928-33
16	543	58.3	117	US-07-534-	Sequence 4, Applicatio	2,928-33
17	543	58.3	117	US-08-477-	Sequence 15, Applicati	2,928-33
18	543	58.3	117	US-08-487-	Sequence 15, Applicati	2,928-33
19	543	58.3	117	US-08-478-	Sequence 15, Applicati	2,928-33
20	543	58.3	117	US-08-474-	Sequence 104, Applicati	2,928-33
21	543	58.3	117	US-08-487-	Sequence 4, Applicatio	2,928-33
22	543	58.3	117	US-08-474-	Sequence 15, Applicati	2,928-33

23	543	58.3	117	US-08-474-	Sequence 72, Applicati	2,938-33
24	543	58.3	117	US-08-474-	Sequence 4, Applicatio	2,938-33
25	543	58.3	117	US-08-477-	Sequence 72, Applicati	2,938-33
26	543	58.3	117	US-08-487-	Sequence 104, Applicati	2,938-33
27	543	58.3	117	US-08-477-	Sequence 4, Applicatio	2,938-33
28	543	58.3	117	US-07-534-	Sequence 72, Applicati	2,938-33
29	543	58.3	117	US-07-634-	Sequence 104, Applicati	2,938-33
30	538	57.8	121	US-08-477-	Sequence 53, Applicati	7,238-33
31	538	57.8	121	US-07-634-	Sequence 53, Applicati	7,238-33
32	538	57.8	121	US-08-487-	Sequence 53, Applicati	7,238-33
33	538	57.8	121	US-08-474-	Sequence 53, Applicati	7,238-33
34	514	55.2	123	PCT-US95-0	Sequence 11, Applicati	5,458-31
35	514	55.2	142	PCT-US95-0	Sequence 17, Applicati	5,458-31
36	502	53.0	140	US-07-246-	Sequence 28, Applicati	4,728-30
37	502	53.0	146	PCT-US95-0	Sequence 155, Applicati	4,728-30
38	502	53.0	146	US-08-276-	Sequence 155, Applicati	4,728-30
39	501	53.8	124	US-08-276-	Sequence 66, Applicati	5,648-30
40	501	53.8	124	PCT-US95-0	Sequence 66, Applicati	5,648-30
41	496	53.3	119	PCT-US95-0	Sequence 10, Applicati	1,398-29
42	495	53.2	98	US-08-311-	Sequence 140, Applicati	1,558-29
43	495	53.2	113	PCT-US95-0	Sequence 12, Applicati	1,668-29
44	492	52.8	124	PCT-US95-0	Sequence 67, Applicati	2,848-29
45	492	52.8	124	US-08-276-	Sequence 67, Applicati	2,848-29

ALIGNMENTS

RESULT 1
ID US-08-217-918-4 STANDARD: PRT: 147 AA.
XX
AC xxxxxx
DI 01-JAN-1900
DE Sequence 4, Application US/08217918.
XX
Sequence 4, Application US/08217918
Patent No. 5506132
GENERAL INFORMATION:
APPLICANT: LAKE, PHILIP
ATTORNEY: CSTERG, LARS
TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
TITLE OF INVENTION: VAPICELLA-ZOSTER VIRUS
NUMBER OF SEQUENCE: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTA, FASTA, FASTA #10, V-Station #1, 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08217,918
FILING DATE: 24-MAR-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO. 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE 147 AA: 10991 MW: 123305 GR:

```

Query Match      64.78, Score 602, DB 13, Length 129;
Best Local Similarity 72.24; Pred. No. 6,85e-38;
Matches 91; Conservative 14; Mismatch 16; Indels 6; Gaps
14b 1 VLVVCSGAFVKKPKSSVKVTKRSGTSSSAISWVQCAPQGLFWMGGIIPTEGTPNY 114
    111 1111111111111111111111111111111111111111111111111
14y 2 VLVVCSGAEVKKPKSSVKVTKRSGTSSSAISWVQCAPQGLFWMGGIIPTEGTPNY 61
    111 1111111111111111111111111111111111111111111111111
14b 60 AKKFGSPVITITDSTAMWSSVSSSNTALYYCAHFERMALNP----FHYWQGT 114
    1111111111111111111111111111111111111111111111111
14y 62 AKKFGSPVITITDSTAMWSSVSSSNTALYYCAHFERMALNP----FHYWQGT 121
    1111111111111111111111111111111111111111111111111
Db 115 LTVSS 120
    111111
Qy 122 LTVSS 127

RESULT 3
ID PCT-US95-01219-45 STANDARD: PRT: 129 AA.
XX AC
XX AC
XX AC
XX AC
XX 01-JAN-1900
XX Sequence 45, Application PCT/US95-01219.
XX
XX Sequence 45, Application PCT/US95-01219
GENERAL INFORMATION:
CC APPLICANT: Bendig, Mary M.
CC APPLICANT: Legier, Olivier J.
CC APPLICANT: Saldanha, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against Insulin
CC TITLE OF INVENTION: Adhesion Molecule VLA-4
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Hourie and Crow
CC STREET: One Market Plaza, Stewart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER PROGRAM: PDP
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/01219
CC FILING DATE: 25-JAN-1995
CC CLASSIFICATION:
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US 08/186,269
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 20,223
CC REFERENCE/DOCKET NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9400
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 45:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 129 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 129 AA: 13930 MW: 96169 CN:

Query Match      62.68, Score 583, DB 13, Length 129;
Best Local Similarity 69.24; Pred. No. 2,13e-36;

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Matches 90: Conservative 11: Mismatches 25: Indels 4: Gaps 4.

Db 1 CQCLV-QSSAEVKKPKSSVSVKVS-KASGVTFTSYVAISWVQAPQGLWGWGWINPYNSET 59
 QY 1 EVALLLEGSSAEVKKPKSSVSVKVS-VLVFSGDIESPYTLQWLQAPQGGPENWGNIIIP-VYNTIP 59

Db 60 NYAKPQCPGPTITADSTSTAYWELSLSEDTAVYVYCAPAPQYSGSGSTYRGRVXFLDYW 119
 QY 60 NYAKPQCPGPTITADSTSTAYWELSLSEDTAVYVYCAPAPQYSGSGSTYRGRVXFLDYW 117

Db 120 CQCLTVTVSS 129
 QY 118 CQCLTVTVSS 127

RESULT 4
 ID PCT-US93-10555-1? STANDARD: PRT: 120 AA.
 XX
 AC xxxxxx
 DT 01-JAN-1900
 XX
 DE
 CC Sequence 13, Application PCT/US9310555.
 CC Sequence 13, Application PCT/US9310555
 CC GENERAL INFORMATION:
 CC APPLICANT: SILVERMAN, GREGG J.
 CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
 CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY PESTICIDED ANTIHERPES
 CC THROUGH
 CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
 CC ATES
 CC TITLE OF INVENTION: THEREOF
 CC NUMBER OF SEQUENCES: 51
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1880 Century Park East - Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-LOS/MS-LOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US93/10555
 CC FILING DATE: 29-OCT-1993
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Howells, Stacy L.
 CC REGISTRATION NUMBER: 34,842
 CC REFERENCE/DOCKET NUMBER: PD-2670
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO. 13:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 120 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: KAS
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1, 120
 CC SEQUENCE 120 AA: 10008 MW: 78866 CN:

Query Match 62.2% Score 579, DB 11, Length 120;
 Best Local Similarity 67.5% Pred. No. 4,40e-36;

Matches 85: Conservative 17: Mismatches 18: Indels 6: Gaps 3:

Db 1 VHLV-QSSAEVKKPKSSVSVKVS-KASGVTFTSYVAISWVQAPQGLWGWGWINPYNSET 59
 QY 2 VQALLLEGSSAEVKKPKSSVSVKVS-QQVFGDIESPYTLQWLQAPQGGPENWGNIIIPVYNTIP 61

Db 60 NYAKPQCPGPTITADSTSTAYWELSLSEDTAVYVYCAPAPQYSGSGSTYRGRVXFLDYW 114
 QY 62 AKRFQPSLSTADSTSTAYWELSLSEDTAVYVYCAPAPQYSGSGSTYRGRVXFLDYW 121

Db 115 LVTVSS 120
 QY 122 LVTVSS 137

RESULT 5
 ID PCT-US95-00067-2 STANDARD: PRT: 122 AA.
 XX
 AC xxxxxx
 DT 01-JAN-1900
 XX
 DE
 CC Sequence 2, Application PCT/US9500067
 CC Sequence 2, Application PCT/US9500067
 CC GENERAL INFORMATION:
 CC APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
 CC TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HERPES
 CC TITLE OF INVENTION: SIMPLEX VIRUS AND METHODS THEREFOR
 CC NUMBER OF SEQUENCES: 25
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Spensley Horn Jubas & Lubitz
 CC STREET: 1880 Century Park East, Suite 500
 CC CITY: Los Angeles
 CC STATE: California
 CC COUNTRY: USA
 CC ZIP: 90067
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: Floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-POS/MS-DOS
 CC SOFTWARE: PatentIn Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: PCT/US95/00067
 CC FILING DATE: 04-JAN-1995
 CC CLASSIFICATION:
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Hallie, Ph.D., Lisa A.
 CC REGISTRATION NUMBER: 38,347
 CC REFERENCE/DOCKET NUMBER: PD-3229
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (619) 455-5100
 CC TELEFAX: (619) 455-5110
 CC INFORMATION FOR SEQ ID NO. 2:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 122 amino acids
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: peptide
 CC IMMEDIATE SOURCE:
 CC CLONE: FdHSV 8
 CC FEATURE:
 CC NAME/KEY: Peptide
 CC LOCATION: 1, 122
 CC SEQUENCE 122 AA: 12999 MW: 86643 CN;

Query Match 60.7% Score 585; DB 13; Length 122;
 Best Local Similarity 66.7% Pred. No. 5,50e-39;
 Matches 82: Conservative 14: Mismatches 26: Indels 1: Gaps 1;

Db 1 LQSSAEVKKPKSSVSVKVS-KASGVTFTSYVAISWVQAPQGLWGWGWINPYNSET 59
 QY 1 LQSSAEVKKPKSSVSVKVS-KASGVTFTSYVAISWVQAPQGLWGWGWINPYNSET 59

QY 5 LEUSGAEVKKPSSSVKVSQVVPQGFPSYIIQLWLPQADPQGPENMGNIPVYNTPNYAK 64
Db 61 FQRLITITAVSTAYMOLSLGTYEDTAMKYCARVAYMLEPTVTAGG-LDVWGOGTIVT 119
QY 65 FQGLSITAGSTAYMELSSLSSELTAVYFCARVVPNAIPHTMAYFLYFWG-LTLVT 124
Db 120 VAS 122
QY 125 VSS 127

RESULT 6
ID US-08-478-039-63 STANDARD: PPT: 128 AA.
XX
AC xxxxxx
DT 01-JAN-1900
XX
DE Sequence 63, Application US/08478039.
XX
CC Sequence 63, Application US/08478039
CC Patent No. 5681722
CC GENERAL INFORMATION:
CC APPLICANT: Newman, Roland A
CC APPLICANT: Hanna, Nabil
CC APPLICANT: Raab, Ronald W.
CC TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
CC NUMBER OF SEQUENCES: 114
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: RUPNS, POANE, SWICKER & MATHIS
CC STREET: 699 Prince St.
CC CITY: Alexandria
CC STATE: VA
CC COUNTRY: USA
CC ZIP: 22313-1404
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: IBM PC Compatible
CC SOFTWARE: Patent In Release #1.0, Version #1.30
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/478,039
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 435
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/379,072
CC FILING DATE: 25-JAN-1995
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/912,202
CC FILING DATE: 10-JUL-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/856,281
CC FILING DATE: 23-MAR-1992
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/735,064
CC FILING DATE: 25-JUL-1991
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Teskin Esq., Robin L.
CC REGISTRATION NUMBER: 35 030
CC REFERENCE/DOCKET NUMBER: 012712-160
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 703-836-6620
CC TELEFAX: 703-836-2021
CC INFORMATION FOR SEQ ID NO: 63:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 128 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: not relevant
CC TOPOLOGY: not relevant
CC MOLECULE TYPE: peptide
CC ORIGINAL SOURCE:
CC ORGANISM: H₂O₂ sapiens
CC POSITION IN GENOME:

CC CHROMOSOME/SEGMENT: VHL consensus
SQ SEQUENCE 128 AA; 14138 MW; 114948 CN;
Query Match 59.2%, Score 551; DR 7; Length 128;
Best Local Similarity 63.3%; Pctid No. 6.93e-44;
Matches 81; Conservative 9; Mismatches 35; Indels 4; Gaps 4;
Db 2 VQLV-QSGAEVKKPSSSVKVSQVVPQGFPSYIIQLWLPQADPQGPENMGNIPVYNTPNY 60
QY 2 VQLV-QSGAEVKKPSSSVKVSQVVPQGFPSYIIQLWLPQADPQGPENMGNIPVYNTPNY 61
Db 51 ALXFGPHVIXIXDXSXNIATMELSSLSSELTAVYFCARVAYMLEPTVTAGG-LDVWGOGTIVT 120
QY 62 AOKFGRLSITADDSITAYMELSSLSSELTAVYFCARV-VI-PNAIRHTMAYFLYFWG 119
Db 121 GLTVTSS 128
QY 120 GLTVTSS 127

RESULT 7
ID PCT-US92-10983-63 STANDARD: PRT: 102 AA.
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AC xxxxxx
DT 01-JAN-1900
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DE Sequence 63, Application PCT/US92/10983.
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CC Sequence 63, Application PCT/US92/10983
CC GENERAL INFORMATION:
CC APPLICANT: Lonberg, Nils
CC APPLICANT: Kay, Robert M.
CC TITLE OF INVENTION: Transgenic Non-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 152
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: William M. Smith
CC STREET: One Market Plaza, Steuart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US92/10983
CC FILING DATE: 19921217
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14543-9-2
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-326-2400
CC TELEFAX: 415-326-2422
CC INFORMATION FOR SEQ ID NO: 63:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 102 amino acids
CC TYPE: AMINO ACID
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 102 AA; 10940 MW; 55781 CN;
Query Match 59.1%, Score 550; DR 10; Length 102;
Best Local Similarity 77.8%; Pctid No. 8.30e-34;
Matches 77; Conservative 9; Mismatches 12; Indels 1; Gaps 1;
Db 5 QVGLV-QSGAEVKKPSSSVKVSQVVPQGFPSYIIQLWLPQADPQGPENMGNIPVYNTPNY 64

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61 YAKRFGQGRVLSITADDSITAYMELSSLSEPSDPTAVYFCAR 99
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RESULT      8
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DE Sequence 53, Application US/08053131.
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XX Sequence 63, Application US/08053131
CC Patent No. 5661016
CC GENERAL INFORMATION.
CC APPLICANT: Kay, Robert M
CC TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for
CC TITLE OF INVENTION: Producing Heterologous Antibodies
CC NUMBER OF SEQUENCES: 197
CC CORRESPONDENCE ADDRESS.
CC ADDRESSEE: Townsend and Townsend Kourie and Crew
CC STREET: One Market Plaza, Stewart Tower, Suite 200
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM.
CC MEDIUM TYPE: Floppy disk
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1 0, Version #1 25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/053,131
CC FILING DATE: 26-APP-1993
CC CLASSIFICATION: 800
CC PRIOR APPLICATION DATA.
CC APPLICATION NUMBER: US 07/990,860
CC FILING DATE: 16-DEC-1992
CC PRIOR APPLICATION DATA.
CC APPLICATION NUMBER: US 07/810,279
CC FILING DATE: 17-DEC-1991
CC PRIOR APPLICATION DATA.
CC APPLICATION NUMBER: US 07/853,408
CC FILING DATE: 18-MAR-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 14643-a-3
CC TELECOMMUNICATION INFORMATION.
CC TELEPHONE: 415-326-3400
CC TELEFAX: 415-326-3420
CC INFORMATION FOR SEQ ID NO: 63.
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 102 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 102 AA; 10340 MW; 55781 CN;

Query Match 59.1% Score 550; DB 7: Length 102;
Best Local Similarity 77.8%; Pred.No. 8.30e-34;
Matches 77: Conservative 9; Mismatches 12; Indels 1; Gaps

Db 5 OVOLV-QSCAEVKKPGSSVKVSCKASGGTSTSSVAISKVPQAGCGLEGWGPILPILGTIAN 63
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64 YAKRFGQGRVTITADKSTISTAYMELSSLSEPSDPTAVYFCAR 102

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01-JAN-1990
Sequence 55, Application PC/TUS9206185.
Sequence 55, Application PC/TUS9206185
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1 0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/06185
FILING DATE: 19910828
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 87654
REFERENCE/DOCKET NUMBER: 14643-5
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
SEQUENCE 102 AA; 10940 MW; 55781 CN;
Query Match 59.1%; Score 550; DB 10; Length 102;
Pest Local Similarity 77.8%; Pred No 8 30e-34;
Matches 77, Conservative 9, Mismatches 22, Indels 1, Gaps 1.
Db 5 QVCLV_QSAEYKKPDSYKVKSCASGDTFFSYAISWVFLAPQVLEWMAHIIILDLIA
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QY 61 YAKFKGVRLTADSTSTAYMELSLRSETAVYFCAR 99
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AC xxxxxx
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DT 01-JAN-1990
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Sequence 55, Application US/07834539A

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XX      01-JAN-1900
XX
XX      Sequence 55, Application PC/TUS9206185.
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XX      Sequence 55, Application PC/TUS9206185
XX      GENERAL INFORMATION:
XX      APPLICANT: Lonberg, Nils
XX      APPLICANT: Kay, Robert M
XX      TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
XX      TITLE OF INVENTION: Producing Heterologous Antibodies
XX      NUMBER OF SEQUENCES: 75
XX      CORRESPONDENCE ADDRESS:
XX      ADDRESSEE: William M. Smith
XX      STREET: One Market Plaza, Stewart Tower, Suite 2000
XX      CITY: San Francisco
XX      STATE: California
XX      COUNTRY: USA
XX      ZIP: 94105
XX      COMPUTER READABLE FORM:
XX      MEDIUM TYPE: Floppy disk
XX      COMPUTER: IBM PC compatible
XX      OPERATING SYSTEM: PC-DOS/MS-DOS
XX      SOFTWARE: Patent In Release #1 0, Version #1.25
XX      CURRENT APPLICATION DATA:
XX      APPLICATION NUMBER: PCT/US92/06185
XX      FILING DATE: 19910828
XX      CLASSIFICATION:
XX      ATTORNEY/AGENT INFORMATION:
XX      NAME: Smith, William M.
XX      REGISTRATION NUMBER: 87654
XX      REFERENCE/DOCKET NUMBER: 14643-5
XX      TELECOMMUNICATION INFORMATION:
XX      TELEPHONE: 415-543-9600
XX      TELEFAX: 415-543-5043
XX      INFORMATION FOR SEQ ID NO: 55:
XX      SEQUENCE CHARACTERISTICS:
XX      LENGTH: 102 amino acids
XX      TYPE: AMINO ACID
XX      TOPOLOGY: linear
XX      STRANDEDNESS: single
XX      MOLECULE TYPE: peptide
XX      SEQUENCE 102 AA; 10940 MW; 55781 CN;
XX
XX      Query Match 59.1%; Score 550; DB 10; Length 102;
XX      Best Local Similarity 77.8%; Pred No. 8 30e-34;
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XX      Sequence 55, Application PC/TUS9206185
XX      GENERAL INFORMATION:
XX      APPLICANT: Lonberg, Nils
XX      APPLICANT: Kay, Robert M
XX      TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
XX      TITLE OF INVENTION: Producing Heterologous Antibodies
XX      NUMBER OF SEQUENCES: 75
XX      CORRESPONDENCE ADDRESS:
XX      ADDRESSEE: William M. Smith
XX      STREET: One Market Plaza, Stewart Tower, Suite 2000
XX      CITY: San Francisco
XX      STATE: California
XX      COUNTRY: USA
XX      ZIP: 94105
XX      COMPUTER READABLE FORM:
XX      MEDIUM TYPE: Floppy disk
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XX      FILING DATE: 19910828
XX      CLASSIFICATION:
XX      ATTORNEY/AGENT INFORMATION:
XX      NAME: Smith, William M.
XX      REGISTRATION NUMBER: 87654
XX      REFERENCE/DOCKET NUMBER: 14643-5
XX      TELECOMMUNICATION INFORMATION:
XX      TELEPHONE: 415-543-9600
XX      TELEFAX: 415-543-5043
XX      INFORMATION FOR SEQ ID NO: 55:
XX      SEQUENCE CHARACTERISTICS:
XX      LENGTH: 102 amino acids
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XX      TOPOLOGY: linear
XX      STRANDEDNESS: single
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XX      Best Local Similarity 77.8%; Pred No. 8 30e-34;
XX      Matches 77, Conservative 9, Mismatches 10, Indels 1, Gaps 1;
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XX      01-JAN-1900
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XX      GENERAL INFORMATION:
XX      APPLICANT: Lonberg, Nils
XX      APPLICANT: Kay, Robert M
XX      TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
XX      TITLE OF INVENTION: Producing Heterologous Antibodies
XX      NUMBER OF SEQUENCES: 75
XX      CORRESPONDENCE ADDRESS:
XX      ADDRESSEE: William M. Smith
XX      STREET: One Market Plaza, Stewart Tower, Suite 2000
XX      CITY: San Francisco
XX      STATE: California
XX      COUNTRY: USA
XX      ZIP: 94105
XX      COMPUTER READABLE FORM:
XX      MEDIUM TYPE: Floppy disk
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XX      OPERATING SYSTEM: PC-DOS/MS-DOS
XX      SOFTWARE: Patent In Release #1 0, Version #1.25
XX      CURRENT APPLICATION DATA:
XX      APPLICATION NUMBER: PCT/US92/06185
XX      FILING DATE: 19910828
XX      CLASSIFICATION:
XX      ATTORNEY/AGENT INFORMATION:
XX      NAME: Smith, William M.
XX      REGISTRATION NUMBER: 87654
XX      REFERENCE/DOCKET NUMBER: 14643-5
XX      TELECOMMUNICATION INFORMATION:
XX      TELEPHONE: 415-543-9600
XX      TELEFAX: 415-543-5043
XX      INFORMATION FOR SEQ ID NO: 55:
XX      SEQUENCE CHARACTERISTICS:
XX      LENGTH: 102 amino acids
XX      TYPE: AMINO ACID
XX      TOPOLOGY: linear
XX      STRANDEDNESS: single
XX      MOLECULE TYPE: peptide
XX      SEQUENCE 102 AA; 10940 MW; 55781 CN;
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XX      Query Match 59.1%; Score 550; DB 10; Length 102;
XX      Best Local Similarity 77.8%; Pred No. 8 30e-34;
XX      Matches 77, Conservative 9, Mismatches 10, Indels 1, Gaps 1;
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XX      APPLICANT: Lonberg, Nils
XX      APPLICANT: Kay, Robert M
XX      TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
XX      TITLE OF INVENTION: Producing Heterologous Antibodies
XX      NUMBER OF SEQUENCES: 75
XX      CORRESPONDENCE ADDRESS:
XX      ADDRESSEE: William M. Smith
XX      STREET: One Market Plaza, Stewart Tower, Suite 2000
XX      CITY: San Francisco
XX      STATE: California
XX      COUNTRY: USA
XX      ZIP: 94105
XX      COMPUTER READABLE FORM:
XX      MEDIUM TYPE: Floppy disk
XX      COMPUTER: IBM PC compatible
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XX      CURRENT APPLICATION DATA:
XX      APPLICATION NUMBER: PCT/US92/06185
XX      FILING DATE: 19910828
XX      CLASSIFICATION:
XX      ATTORNEY/AGENT INFORMATION:
XX      NAME: Smith, William M.
XX      REGISTRATION NUMBER: 87654
XX      REFERENCE/DOCKET NUMBER: 14643-5
XX      TELECOMMUNICATION INFORMATION:
XX      TELEPHONE: 415-543-9600
XX      TELEFAX: 415-543-5043
XX      INFORMATION FOR SEQ ID NO: 55:
XX      SEQUENCE CHARACTERISTICS:
XX      LENGTH: 102 amino acids
XX      TYPE: AMINO ACID
XX      TOPOLOGY: linear
XX      STRANDEDNESS: single
XX      MOLECULE TYPE: peptide
XX      SEQUENCE 102 AA; 10940 MW; 55781 CN;
XX
XX      Query Match 59.1%; Score 550; DB 10; Length 102;
XX      Best Local Similarity 77.8%; Pred No. 8 30e-34;
XX      Matches 77, Conservative 9, Mismatches 10, Indels 1, Gaps 1;
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XX      Sequence 55, Application PC/TUS9206185
XX      GENERAL INFORMATION:
XX      APPLICANT: Lonberg, Nils
XX      APPLICANT: Kay, Robert M
XX      TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
XX      TITLE OF INVENTION: Producing Heterologous Antibodies
XX      NUMBER OF SEQUENCES: 75
XX      CORRESPONDENCE ADDRESS:
XX      ADDRESSEE: William M. Smith
XX      STREET: One Market Plaza, Stewart Tower, Suite 2000
XX      CITY: San Francisco
XX      STATE: California
XX      COUNTRY: USA
XX      ZIP: 94105
XX      COMPUTER READABLE FORM:
XX      MEDIUM TYPE: Floppy disk
XX      COMPUTER: IBM PC compatible
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XX      SOFTWARE: Patent In Release #1 0, Version #1.25
XX      CURRENT APPLICATION DATA:
XX      APPLICATION NUMBER: PCT/US92/06185
XX      FILING DATE: 19910828
XX      CLASSIFICATION:
XX      ATTORNEY/AGENT INFORMATION:
XX      NAME: Smith, William M.
XX      REGISTRATION NUMBER: 87654
XX      REFERENCE/DOCKET NUMBER: 14643-5
XX      TELECOMMUNICATION INFORMATION:
XX      TELEPHONE: 415-543-9600
XX      TELEFAX: 415-543-5043
XX      INFORMATION FOR SEQ ID NO: 55:
XX      SEQUENCE CHARACTERISTICS:
XX      LENGTH: 102 amino acids
XX      TYPE: AMINO ACID
XX      TOPOLOGY: linear
XX      STRANDEDNESS: single
XX      MOLECULE TYPE: peptide
XX      SEQUENCE 102 AA; 10940 MW; 55781 CN;
XX
XX      Query Match 59.1%; Score 550; DB 10; Length 102;
XX      Best Local Similarity 77.8%; Pred No. 8 30e-34;
XX      Matches 77, Conservative 9, Mismatches 10, Indels 1, Gaps 1;
01  YACKFCPLSITADDSISTAYMELSLRSEDVAVYFCAR 99
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PCT-US92-06185-55      STANDARD;      PRT;      102 AA.
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XX      Sequence 55, Application PC/TUS9206185.
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XX      GENERAL INFORMATION:
XX      APPLICANT: Lonberg, Nils
XX      APPLICANT: Kay, Robert M
XX      TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
XX      TITLE OF INVENTION: Producing Heterologous Antibodies
XX      NUMBER OF SEQUENCES: 75
XX      CORRESPONDENCE ADDRESS:
XX      ADDRESSEE: William M. Smith
XX      STREET: One Market Plaza, Stewart Tower, Suite 2000
XX      CITY: San Francisco
XX      STATE: California
XX      COUNTRY: USA
XX      ZIP: 94105
XX      COMPUTER READABLE FORM:
XX      MEDIUM TYPE: Floppy disk
XX      COMPUTER: IBM PC compatible
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XX      CURRENT APPLICATION DATA:
XX      APPLICATION NUMBER: PCT/US92/06185
XX      FILING DATE: 19910828
XX      CLASSIFICATION:
XX      ATTORNEY/AGENT INFORMATION:
XX      NAME: Smith, William M.
XX      REGISTRATION NUMBER: 87654
XX      REFERENCE/DOCKET NUMBER: 14643-5
XX      TELECOMMUNICATION INFORMATION:
XX      TELEPHONE: 415-543-9600
XX      TELEFAX: 415-543-5043
XX      INFORMATION FOR SEQ ID NO: 55:
XX      SEQUENCE CHARACTERISTICS:
XX      LENGTH: 102 amino acids
XX      TYPE: AMINO ACID
XX      TOPOLOGY: linear
XX      STRANDEDNESS: single
XX      MOLECULE TYPE: peptide
XX      SEQUENCE 102 AA; 10940 MW; 55781 CN;
XX
XX      Query Match 59.1%; Score 550; DB 10; Length 102;
XX      Best Local Similarity 77.8%; Pred No. 8 30e-34;
XX      Matches 77, Conservative 9, Mismatches 10, Indels 1, Gaps 1;
01  YACKFCPLSITADDSISTAYMELSLRSEDVAVYFCAR 99
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PCT-US92-06185-55      STANDARD;      PRT;      102 AA.
AC      xxxxxx
XX      01-JAN-1900
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XX      Sequence 55, Application PC/TUS9206185.
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XX      Sequence 55, Application PC/TUS9206185
XX      GENERAL INFORMATION:
XX      APPLICANT: Lonberg, Nils
XX      APPLICANT: Kay, Robert M
XX      TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
XX      TITLE OF INVENTION: Producing Heterologous Antibodies
XX      NUMBER OF SEQUENCES: 75
XX     
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[illegible]

Thu Feb 26 07:04:44 1998

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CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002600
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 104:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE: 117 AA; 12472 MW; 77871 CN;

Query Match 58.3%; Score 543; DB 6; Length 117;
Best Local Similarity 76.5%; Pred No 2 93e-33;
Matches 75; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

Db 1 QVQLV-OSGAEVKPGSSVKVSKASGTFSSRAIIWVRQAPGQGLEWMGGIVPMFGPPN 59
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RESULT 15
ID US-08-487-200-72 STANDARD: PPT: 117 AA.
XX xxxxxx
AC AC
DT 01-JAN-1900
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DE Sequence 72, Application US/08487200.
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CC Sequence 72, Application US/08487200
CC Patent No. 5693762
CC GENERAL INFORMATION:
CC APPLICANT: QUEEN, Cary L.
CC APPLICANT: CO, Man Sung
CC APPLICANT: SCHNEIDER, William P.
CC APPLICANT: LANDOLFI, Nicholas F.
CC APPLICANT: GOELINGH, Kathleen L.
CC APPLICANT: SELICK, Harold E.
CC TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
CC NUMBER OF SEQUENCES: 113
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend and Crew
CC STREET: 379 Lytton Avenue
CC CITY: Palo Alto
CC STATE: California
CC COUNTRY: US
CC ZIP: 94301
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: PatentIn Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/487,200
CC FILING DATE: 7-JUN-1995
CC CLASSIFICATION: 424
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CC APPLICATION NUMBER: US 07/634,278
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CC APPLICATION NUMBER: US 07/590,274
CC FILING DATE: 28-SEP-1990
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/310,252
CC FILING DATE: 13-FEB-1989
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/290,975
CC FILING DATE: 28-DEC-1988
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William M
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCKET NUMBER: 11823-002610
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (415) 326-2400
CC TELEFAX: (415) 326-2422
CC INFORMATION FOR SEQ ID NO: 72:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 117 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide
CC SEQUENCE: 117 AA; 12472 MW; 77871 CN;

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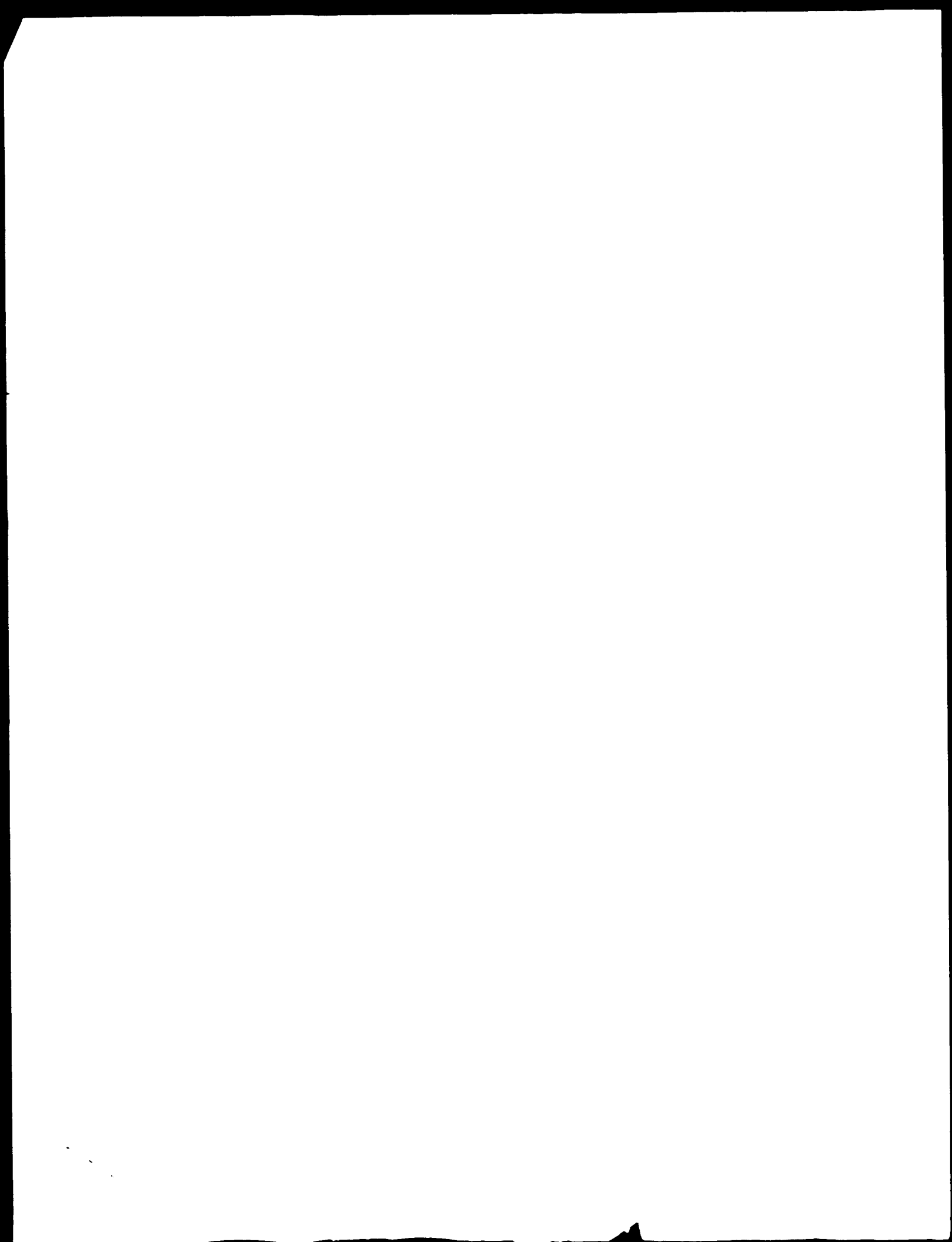
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Job time : 14 secs.

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N 95287497 MEDLINE
 DN 95287497
 TI Occurrence of antibodies reactive with more than one variant of the
 AU Scarselli E; Cerino A; Esposito G; Salini E; Mondelli M U;
 CS Istituto di Ricerche di Biologia Molecolare P. Angeletti (IRBM),
 Rome, Italy.
 NC A131783 (NIAID)
 P30 A128691 (NIAID)
 P30A06516 (NCI)
 SO JOURNAL OF VIROLOGY, (1995 JUL) 69 (7) 4407-12.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 ES Cancer Journals; Priority Journals
 OS GENBANK-X79671; GENBANK-X79672; GENBANK-X79673
 EM 199509
 AB The hepatitis C virus (HCV) is a frequent cause of chronic liver
 disease. A mechanism proposed as being responsible for virus
 persistence is evasion of the host immune response through a high
 mutation rate in crucial regions of the viral genome. We have
 sequenced the hypervariable region 1 (HVR1) of the virus isolated
 from three serum samples, collected during 18 months of follow-up,
 from an asymptomatic HCV-infected patient. A synthetic peptide of 27
 amino acids, corresponding to the HVR1 sequence found to be
 predominant in both the second and third samples, was used as the
 antigen for detection of antibodies by enzyme-linked immunosorbent
 assay (ELISA). We observed reactivity against this HVR1 sequence in
 the first serum sample before the appearance of the viral isolate in
 the bloodstream; the reactivity increased in the second and third
 samples while the cognate viral sequence became predominant.
 Moreover, our results show that antibodies from all three samples
 recognize a region mapping at the carboxyl-terminal part of the HVR1
 and are cross-reactive with the HVR1 sequence previously found in
 the same patient. The presence of anti-HVR1 antibodies was
 investigated in a further 142 HCV patients: 141 viremic and 21
 nonviremic. Two synthetic peptides were used, the first
 corresponding to the sequence derived from the patient described
 above and the second one synthesized according to the sequence of
 the HCV BK strain. A high frequency of positive reactions against
 both HVR1 variants was detected in the samples from the viremic
 individuals. Finally, antibodies cross-reactive with both variants
 were shown to be present by competitive ELISA in 6 of 10 viremic
 patients. The potential negative implications of this observation
 for the host are discussed.



L2 ANSWER 1 OF 15 MEDLINE
 AN 1998229450 MEDLINE
 DN 98229450
 TI Antibodies directed to envelope proteins of hepatitis C virus
 AU Lechner SF; Rispeter K; Meisel H; Kraas W; Jung S; Roggendorf M;
 Zibert A
 CS Institut für Virologie, Universitätsklinikum, Essen, Germany.
 SO VIROLOGY, (1998 Apr 10) 243 (2) 313-21.
 Journal code: XEA, ISSN: 0042-6822.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals; Cancer Journals
 EM 199807
 EW 19980705
 AB The relatively high variability of the hepatitis C virus (HCV) envelope proteins E1 and E2 suggests that parts of these proteins other than the hypervariable region 1 (HVR1) might be involved in the induction of virus neutralizing antibodies. To test this hypothesis, two HCV proteins, pE1 and pE2 delta, were generated by in vitro translation. They represent amino acids 174-337 of E1 and 411-658 of E2, respectively, of isolate HCV-AD78; the protein pE2 delta contained no HVR1. As a control, protein pC-HVR1, which represents amino acids 384-410 of HVR1 of isolate HCV-AD78, was expressed separately. These three proteins were used in an immunoprecipitation assay to detect the presence of antiviral antibodies in sera of patients infected with the same isolate of HCV (HCV-AD78). Sera were obtained 4-8 months postinfection from patients who later resolved an acute infection or developed chronic liver disease. A high prevalence of antibodies (up to 35.7%) against pE1 and pE2 delta could be detected in both groups of patients, suggesting that these forms of the HCV envelope proteins contain B-cell epitopes. The antibody responses against proteins pE1 and pE2 delta did not differ significantly between patients with resolving or chronic infection, whereas antibodies against protein pC-HVR1 were associated with resolution of infection. Rabbit antisera raised against pE1 and pE2 delta were tested for their ability to neutralize the binding of HCV to susceptible cells in tissue cultures. The results suggested that although a few B-cell epitopes outside of HVR1 can induce virus neutralizing antibodies, these antibodies are probably not associated with the resolution of infection.

L2 ANSWER 3 OF 15 MEDLINE
 AN 1998010011 MEDLINE
 DN 98010011
 TI Characterization of antibody response to hepatitis C virus protein E2 and significance of hypervariable region 1-specific antibodies in viral neutralization.
 AU Zibert A; Dudziak B; Schreier B; Roggendorf M
 CS Institut für Virologie, Universitätsklinikum Essen, Federal Republic of Germany.
 SO ARCHIVES OF VIROLOGY, 1997; 142 (3) 523-34.
 Journal code: 8L7, ISSN: 0304-8568.
 CY Austria
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English



Antibodies directed against hypervariable region 1 (HVR1) of hepatitis C virus (HCV) have recently been shown to neutralize the corresponding HCV isolate *in vitro*. We analyzed the appearance of antibodies directed to HVR1 during the course of infection in a large group of patients who have been infected by the same isolate of a HCV contaminated anti-D immunoglobulin (HCV-AD78). An enzyme-linked immunosorbent assay (ELISA) was established using a synthetic peptide to detect antibodies against the main HVR1 variant of HCV-AD78. 107 sera obtained at different time points post infection (p.i.) of 51 patients having either acute self-limiting (n = 28) or chronic infection (n = 79) were studied. Antibodies directed to HVR1 were found at least at one time point during the infection course in 19 of 28 patients (68%) having acute self-limiting infections and in 17 of 79 patients (21%) with chronic disease. The time of appearance of anti-HVR1 was significantly different between these two patient groups (p = .025) although appearance and titers of other HCV-specific antibodies were found to be similar at early time points p.i. In acute self-limiting infections 9 of 11 sera (82%) of respective patients with sera available within the first 6 months p.i. were anti-HVR1 positive. The highest prevalence of anti-HVR1 in this group of patients was within month 6 to 12 p.i. (64%). None of the sera available after 24 months p.i. had such antibodies. In contrast, only 2 of 15 sera (13%) of chronically infected patients with respective time points of sera were anti-HVR1 positive within the first 6 months p.i. and only 5 of 13 sera (38%) were positive within month 7 to 12 p.i. Seven patients with chronic HCV infections showed at least two consecutive anti-HVR1 negative early time points up to month 18 p.i. Prevalence of anti-HVR1 after 24 months p.i. was high (84%) in this group of patients and most of the patients

Antibodies directed against hypervariable region 1 (HVR1) within the viral glycoprotein E2 of hepatitis C virus (HCV) are postulated to neutralize virus. An *in vitro* infection/binding assay of human fibroblast cells was established in order to study neutralization of HCV, occurrence of mutations in the nucleotide sequence of HVR1 as compared to the inoculum after infection of human fibroblasts suggested replication of HCV in these cells. The significance of HVR1-specific antibodies in sera of patients who were infected in a single-source outbreak by an HCV contaminated anti-D immunoglobulin (IgG) preparation was studied. Using immunoprecipitation and ELISA, HVR1-specific antibodies could be detected in most of the sera obtained early (< or = 1 year p.i.) and late (up to 14 years p.i.) in single patients. Further characterization of the HVR1-specific antibodies in patient sera by attachment studies of HCV to the human fibroblasts suggested that HVR1-specific antibodies in sera obtained early p.i. can neutralize virus of the anti-D IgG preparation.

ANSWER 4 OF 15 MEDLINE
 97286278 MEDLINE
 97286278
 DN
 97286278
 TI Early antibody response against hypervariable region 1 is associated with acute self-limiting infections of hepatitis C virus.
 AU Zibert A; Meisel H; Kraas W; Schulz A; Jung G; Roggendorf M
 CS Institut für Virologie, Universitätsklinikum Essen, Germany.
 SO HEPATOLOGY, (1997 May) 25 (5) 1245-9.
 CY United States
 DT Journal; Article; (JOURNAL ARTICLE)
 LA English
 FS Priority Journals
 EM 199707
 EW 19970709
 AB

FS Priority Journals; Cancer Journals
 EM 199801
 EW 19980104
 AB



maintained high levels of anti-HVRI for up to 17 years p.i. Our findings suggest clearance of virus by respective neutralizing antibodies resulting in a self-limiting infection and may have implications for prognosis of the disease and also for any future vaccine development.

Epitope mapping of antibodies directed against hypervariable region 1 in acute self-limiting and chronic infections due to hepatitis C virus.

Zibert A; Kraas W; Meisel H; Jung G; Roggendorf M
 Institut für Virologie, Universitätsklinikum Essen, Germany.
 JOURNAL OF VIROLOGY, (1997 May) 71 (5) 4123-7.
 Journal code: JCV, ISSN: 0022-538X.
 United States
 Journal: Article; (JOURNAL ARTICLE)
 English
 Priority Journals: Cancer Journals
 EM 199707
 EW 19970701
 AB

Epitopes of hypervariable region 1 (HVRI) were mapped by enzyme-linked immunosorbent assay using follow-up sera of patients, all of whom were infected with the same isolate of hepatitis C virus (HCV). Our results suggest that (i) an early appearance (up to month 13 postinfection) of antibodies directed to the N terminus of HVRI is associated with acute self-limiting infections of HCV and (ii) isolate-independent antibodies which are mainly directed to the C terminus of HVRI seem to persist in chronically infected patients. The relevance of HVRI-specific antibodies for neutralization was evaluated by characterization of a rabbit serum.

=> p bib, ab 6

Zibert A; Schreier E; Roggendorf M
 Institute of Virology, University of Essen, Germany.
 VIROLOGY, (1995 Apr 20) 208 (2) 653-61.
 Journal code: XEA, ISSN: 0042-6822.
 United States
 Journal: Article; (JOURNAL ARTICLE)
 English
 Priority Journals: Cancer Journals
 EM 199503
 AB

It has been postulated that antibodies specific to the hypervariable region 1 (HVRI) within the putative envelop protein E2 of hepatitis C virus (HCV) can neutralize virus. We studied such antibodies in sera of patients who were infected in a single-source outbreak by a contaminated anti-D immunoglobulin preparation (HCV-AD78). The nucleotide sequences of cDNAs encoding HVRI of HCV-AD78 were determined. The four major variants (HVRI-A, B, C, and D) were expressed as fusion proteins in *Escherichia coli*. Sixty-seven percent of sera contained antibodies to HVRI-A. Sera unrelated to infection of the outbreak also recognized HVRI-A but to a lesser extent (13%), suggesting that not all HVRI-specific antibodies are absolutely isolate-specific. Antibodies directed against individual variants of HVRI were found in sera obtained early postinfection (p.i.) (< or = 1 year) but also in sera obtained several years later. An in vitro binding assay of HCV to tissue culture cells was

LC ANSWER 5 OF 15 MEDLINE
 AN 97048466 MEDLINE
 DN 97048466
 TI Epitope mapping of antibodies directed against hypervariable region 1 in acute self-limiting and chronic infections due to hepatitis C virus.
 AU Zibert A; Kraas W; Meisel H; Jung G; Roggendorf M
 Institut für Virologie, Universitätsklinikum Essen, Germany.
 JOURNAL OF VIROLOGY, (1997 May) 71 (5) 4123-7.
 Journal code: JCV, ISSN: 0022-538X.
 United States
 Journal: Article; (JOURNAL ARTICLE)
 English
 Priority Journals: Cancer Journals
 EM 199707
 EW 19970701
 AB

LC ANSWER 6 OF 15 MEDLINE
 AN 97066271 MEDLINE
 DN 97066271
 TI Antibodies in human sera specific to hypervariable region 1 of hepatitis C virus can block viral attachment.
 AU Zibert A; Schreier E; Roggendorf M
 Institute of Virology, University of Essen, Germany.
 VIROLOGY, (1995 Apr 20) 208 (2) 653-61.
 Journal code: XEA, ISSN: 0042-6822.
 United States
 Journal: Article; (JOURNAL ARTICLE)
 English
 Priority Journals: Cancer Journals
 EM 199503
 AB



employed to further characterize these sera. Five of seven sera that were obtained early p.i. prevented binding of HCV to cells. Preincubation of such sera with HVR1-specific fusion proteins restored binding of HCV to cells in four of five sera. These findings suggest that the majority of neutralizing antibodies are directed against HVR1.

AC	T371d1;
AD	14-APR-1997 (first entry)
DE	DNA fragment vk65.5, containing variable kappa chain gene.
DM	Variable; kappa chain; gene segment; human; DNA fragment; vk65.5;
KW	unrearranged; light chain; minilocus; transgene; transgenic; mouse;
KW	production; heterologous; antibody; gamma; immunoglobulin; ss.
KS	Homo sapiens.
FH	Key Location/Qualifiers
FT	exon 180..229
FT	/tag= a 398..693
FT	exon /tag= b
FN	US5545806-A.
PD	13-AUG-1996.
PF	29-AUG-1990: 574748.
PR	29-AUG-1990: US-574748.
PR	31-AUG-1990: US-575962.
PR	17-DEC-1991: US-810279.
PR	18-MAR-1992: US-853408.
FR	23-JUN-1992: US-904068
PA	16-DEC-1992: US-990860
PA	(GENP-) GENPHARM INT INC.
PI	Kay RM, Lomberg N;
DR	WPI: 96-383736/38.
DR	p-FSDB. W03947.
PT	Prodn. of heterologous human immunoglobulin(s) - by immunising
PT	transgenic mice
PS	Example 21: Fig 42: qapp: English
CC	The present sequence is the variable kappa chain gene segment
CC	containing human DNA fragment, vk65.5, which was co-injected along
CC	with the human DNA fragments vk65.3, vk65.8 and vk65.15 into half
CC	day mouse embryo pronuclei, to generate an unrearranged light chain
CC	minilocus transgene. The resulting transgenic mice can be used for
CC	the production of heterologous (i.e. human) antibodies against
CC	specific antigens, this comprises immunising a mouse with a
CC	preselected antigen and collecting antigen binding heterologous
CC	human gamma immunoglobulins.
SC	sequence 900 BP: 225 A.
SC	244 C. 204 G. 227 T:

QY 67 GCCAGTCAAGATGTTTCACCTGGTAACTG

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 AC Q92546;
 DT 11-MAR-1996 (first entry)
 DE pComb3 expression vector.
 KW pComb3; phagemid expression phase; coat protein; cpIII; cp3;
 KW Gene III; filamentous phase; minor phase coat protein; cpIII; cp3;
 KW bacterial membrane; periplasm; E. coli; human; Fab; HIV; gp120;
 KW recombinatorial Fab library; cassette; Fd/cp3; lacZ promoter/operator;
 KW ribosome binding site; RBS; PelB leader; spacer; tether sequence;
 KW MT4; pMT4-3; antibody; ss: cyclic.
 KW Synthetic.
 PN W09511317-Al.
 PD 27-APR-1995.
 PE 19-OCT-1994; U11907.
 PF 19-OCT-1993; US-139409.
 PR 26-APR-1994; US-233619.
 PS 19-SEP-1994; US-308841.
 PA (SCRI) SRIEPPS.RES INST.
 PI Barbas CF, Burton DR, Lerner RA;
 WP1, 95-170233/22.
 DR Synthesis of human neutralising monoclonal antibodies to human
 PT Immunodeficiency virus - used for diagnosis and immuno-therapy of
 PT HIV-induced disease
 PS Example 1; Page 185-188; 249pp; English.
 CC This sequence represents the pComb3 phagemid expression vector. This
 CC vector has been designed to allow for anchoring of expressed proteins on
 CC the bacteriophage coat protein 3. Gene III of filamentous phase encodes
 CC the 406 residue minor phase coat protein, cpIII (cp3), which is expressed
 CC prior to extrusion in the phase assembly process on the periplasm of E.
 CC coli. This plasmid was used within the scope of the invention to express
 CC various mutagenised human Fab's. pComb3 allows for both surface display
 CC regions which bind to HIV gp120. The vector was designed for the cloning
 CC and soluble forms of the Fabs. The vector consists of a DNA molecule having
 CC of combinatorial Fab libraries. pCumb consists of a DNA molecule having
 CC two cassettes to express one fusion protein, Fd/cp3, and one soluble
 CC protein, the light chain. The finished vector comprises, operatively
 CC linked 5' to 3', a first cassette consisting of lacZ promoter/operator
 CC sequences, a NotI restriction site, a cloning region bordered by 5' XhoI and
 CC pelB leader, a spacer region, a cloning region bordered by 5' XhoI and
 CC bacteriophage cp3 followed by a stop codon, a NheI restriction site,
 CC between the two cassettes, and a second lacZ promoter/operator sequence,
 CC followed by an expression control RBS, a pelB leader, a spacer region,
 CC cloning region bordered by 5' SacI and 3' XbaI restriction sites,
 CC followed by expression control stop sequences and a second NotI
 CC restriction site. The pComb3 expression vector forms the basic construct
 CC of the M74 fab display phagemid expression vector, pMT4-3 (see also
 CC Q92540), used in the invention for the production of synthetic human Fab
 CC antibodies against gp120 of HIV.
 CC Sequence 4691 BP: 1171 C, 1232 G, 1118 T;
 SQ

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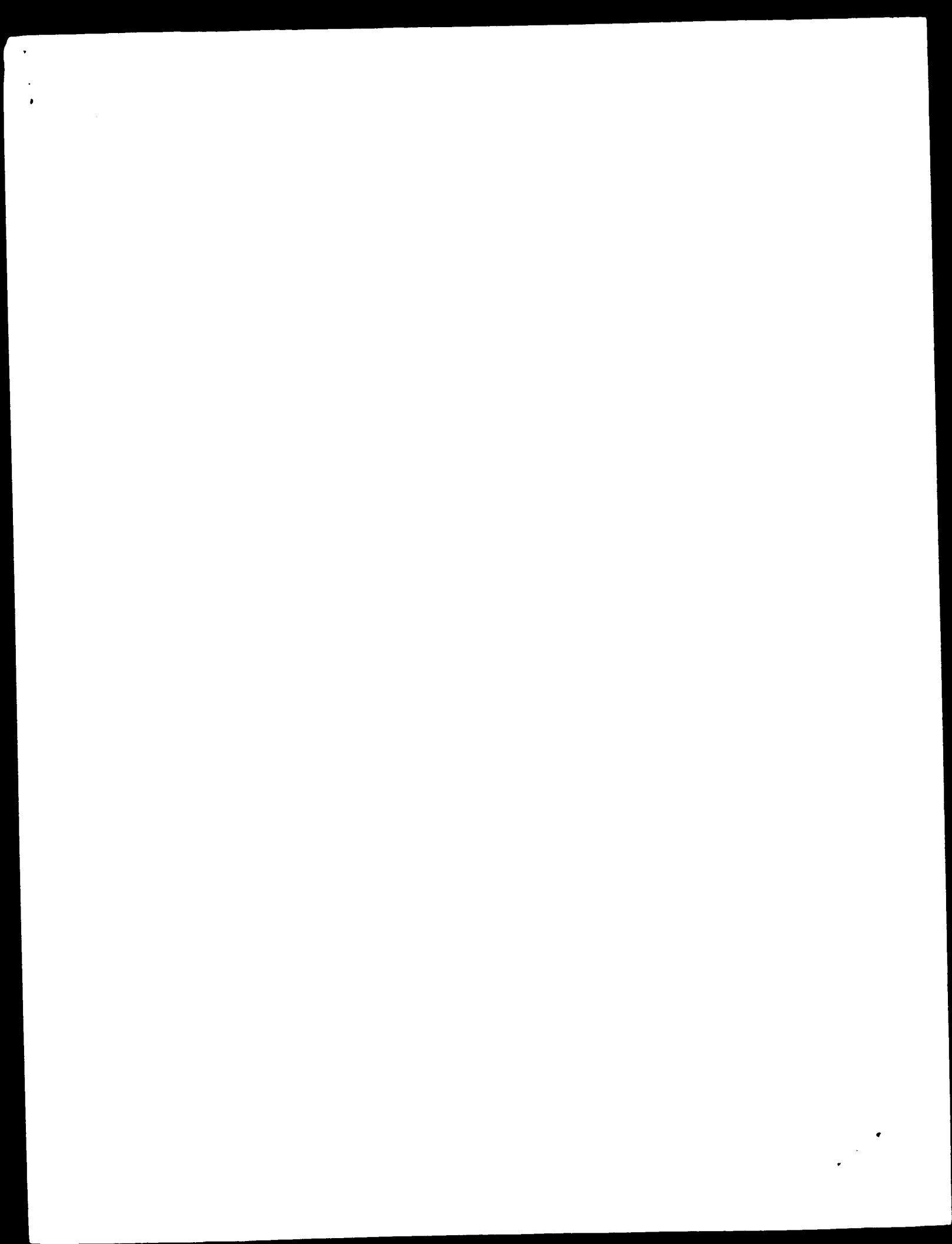
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US-08-844-215-16.rng

Page 9

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REFERENCE 1 (bases 1 to 823)
 AUTHORS Marra, M., Hillier, L., Allen, M., Howles, M., Dietrich, N., Dubouque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, K. and Waterston, K.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)

COMMENT
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LLM: contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:379418
 Putative full length read
 vector to vector length is 867
 Seq primer: -28M13 rev2 from Amerham
 High quality sequence stop: 492

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 SOURCE pig
 ORGANISM Sus scrofa
 Eukaryotes; mitochondrial eukaryotes; Metazoa; Chordata; Vertebrata; Eutheria; Artiodactyla; Suiformes; Suina; Suidae; Sus.
 REFERENCE 1 (bases 1 to 330)
 AUTHORS Winteroe, A. K., Fredholm, M. and Davies, W.
 TITLE Evaluation and characterization of a porcine small intestine cDNA library
 JOURNAL Mamm. Genome 7, 509-517 (1996)
 REFERENCE 2 (bases 1 to 330)
 AUTHORS Winteroe, A. K.
 TITLE Direct Submission
 JOURNAL Submitted (26-JUL-1995) Winteroe, A. K., The Royal Veterinary and Agricultural University, Department of Animal Science and Animal Health, Division of Animal Genetics, Bulowsovej 13, 1870 Frederiksberg C, DENMARK
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 Db 178 ccagggaaggggtgaggtggtggtggtggtggtggtggtggtggtggtggtggt 237
 QY 121 CCTGGACAGGCTGTGAGTGGATGGAGGATATACCTCTA-TGTTGGAGACACCAACTA 180
 Db 238 ccagactctgaggagagcagctacatttccagctatgccatgtcttgggttccgagact 297
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RESULT 7
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 DEFINITION IG HEAVY CHAIN V-III REGION (HUMAN).
 ACCESSION H73816
 NID g1046750
 KEYWORDS EST.
 SOURCE human clone-214441 primer-M13R1 library-Soares total liver spleen
 INFLS vector-pT73D (Pharmacia) with a modified polylinker
 host=DH10B (ampicillin resistant) Ks102-Pac 1 Ks102-Eco RI Liver
 and spleen from a 20 week-old conception male fetus 1st strand
 cDNA was primed with a Pac 1 - oligo(dT) primer [5',
 AACTGGAAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'], double-stranded
 cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac

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Thu Feb 26 07:05:51 1998

US-08-844-215-27.rsta

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Search completed: Tue Feb 24 13:29:00 1998
Job time : 587 secs.

MILES

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MPSrch_PP protein - protein database search, using Smith-Waterman algorithm

Run on Tue Feb 24 07:03:16 1998. Maspar time 6.87 Seconds
266 870 Million cell updates/sec

Title: >US-08-844-215-1
Description: (1-132) from US0884215.pcp
Perfect Score: 956
Sequence: 1 EVOLLEQSGAEVKEPKGVSK.....RCYPGFQWGGTLVTYSS 132

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13989129 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq30
1:part1 2:part3 3:part4 5:part5 6:part6 7:part7
8:part8 9:part10 11:part12 12:part13 13:part14
14:part15 16:part17 18:part19
19:part20 21:part22 23:part23

Statistics: Mean 30.964; Variance 153.640; scale 0.202

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	696	72.8	481	5	Sequence of antibody	1.37e-47
2	559	58.5	120	9	SpA-reactive IgM heavy	4.30e-36
3	557	58.3	476	6	Antibody D heavy chain	6.32e-36
4	549	57.4	123	23	CEA-specific antibody	2.94e-35
5	537	56.2	98	12	Dp10 VH region.	2.94e-34
6	534	55.9	123	23	CEA-specific antibody	5.23e-34
7	533	55.8	123	23	CEA-specific antibody	6.34e-34
8	532	55.6	123	23	CEA-specific antibody	7.63e-34
9	530	55.4	123	23	CEA-specific antibody	1.13e-33
10	529	55.3	147	12	93KA9 anti-Varicella	1.37e-33
11	526	55.0	110	23	Anti-melanoma antibody	2.43e-33
12	521	54.5	124	9	Monoclonal antibody G	6.32e-33
13	515	53.9	98	12	HV1962 VH region	2.08e-32
14	515	53.9	117	4	Protein encoded by th	2.08e-32
15	515	53.9	117	4	Human heavy chain V	2.08e-32
16	515	53.9	117	20	DNA fragment vH49 8,	2.00e-32
17	515	53.9	122	14	HSV-neutralising anti	2.00e-32
18	513	53.7	120	9	SpA-reactive IgM heavy	2.93e-32
19	512	53.6	121	14	Humanised mouse IgG2	2.54e-32
20	512	53.6	140	9	DPEN-200 Humanised an	3.54e-32

21	511	53.5	145	22	W23841	Human anti-tumour ant	4.25e-32
22	506	52.9	143	23	W21847	Humanised heavy chain	1.13e-31
23	505	52.9	142	9	P50189	Heavy chain variable	1.75e-31
24	503	52.6	249	14	P77610	Humanised 5G1.1 VH +	1.98e-31
25	494	51.7	142	9	P50194	Heavy chain variable	1.11e-30
26	492	51.5	249	14	P77615	Humanised 5G1.1 VH +	1.52e-30
27	489	51.2	117	2	R24104	Human antibody Eu hea	2.88e-30
28	489	51.2	118	3	P29742	Heavy chain variable	2.88e-30
29	489	51.2	248	14	P77607	Humanised anti-grafted	2.99e-30
30	489	51.2	248	14	P77615	Humanised anti-grafted	2.99e-30
31	489	51.2	249	14	R77611	Humanised 5G1.1 VH +	2.88e-30
32	488	51.0	140	23	W21849	Humanised heavy chain	3.48e-30
33	488	51.0	242	7	P93267	Humanised 4G1 Ig hea	3.48e-30
34	488	51.0	235	7	P32568	Humanised 4G1 Ig hea	3.48e-30
35	488	51.0	449	7	R43339	Completely humanised	3.48e-30
36	487	50.9	102	5	P25325	Hv region of human m	4.22e-30
37	487	50.9	468	5	R28808	pre-9A8 humanised hea	4.22e-30
38	482	50.5	131	5	P25724	Humanised VH region	9.05e-29
39	482	50.4	139	11	P62679	CV1748PHA VH region	1.09e-29
40	481	50.3	140	23	K23860	Humanised heavy chain	1.32e-29
41	479	50.1	139	8	R43693	p81.3/Humanised heavy	1.64e-29
42	479	50.1	139	11	P62680	CV1748PHA VH region	1.64e-29
43	478	50.0	139	8	R43689	CV1748PHA VH region	2.35e-29
44	478	50.0	139	11	R62678	Humanised W291 antibo	2.35e-29
45	478	50.0	279	19	W05826		

ALIGNMENTS

RESULT	ID	R24442 standard; Protein: 481 AA.	Location/Qualifiers
AC	R24442		
DE	02-JAN-1992 (first entry)		
DE	Sequence of antibody molecule IgG1.		
KW	Antibody; immunoglobulin G1.		
OS	Homo sapiens.		
FT	Key		
FT	Misc difference 308		
FT	/label= N		
FT	/note= "Substn. to create glycan addition site"		
FT	Misc difference 310		
FT	/label= S		
FT	/note= "see above"		
FT	Misc difference 321		
FT	/label= N		
FT	/note= "see above"		
FT	Misc difference 329		
FT	/label= N		
FT	/note= "see above"		
FT	Misc difference 331		
FT	/label= S		
FT	/note= "see above"		
FT	Misc difference 356		
FT	/label= N		
FT	/note= "see above"		
FT	Misc difference 369		
FT	/label= N		
FT	/note= "see above"		
FT	W09209293-A.		
PD	11-JUN-1992.		
FF	18-NOV-1991. W08605.		
PR	22-NOV-1990; US-618314.		
PA	(GEHO) GEN HOSPITAL CORP.		
PI	Seed B, Walz G.		
DE	WFI 92-016789/26.		
DR	WFSB; Q25443.		
PI	Inhibition of cell adhesion mediated through EAM-1 mol. binding		
PI	- used in treating chronic inflammation, rheumatoid arthritis,		
PT	psoriasis, etc.		
PS	Disclosure, Fig 1, 4pp, English.		
CC	The IgG1 in its nascent form, bears no stably-fixed chains. The		
CC	invariants designed a molecule including several such sites for		
CC	attachment of stably-fixed chains (see R24442, FT). The		

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CC additional N-linked glycosylation sites are introduced at locations
 CC which impair complement fixing and Fc receptor binding ability. They
 CC are preferably located in the CH2 region of the Ig molecule.
 CC Antibodies bearing multiple sialyl-Lex determinants are useful for
 CC disrupting undesirable interactions between cells or proteins.
 CC Disrupting this interaction has therapeutic applications, for
 CC example, in minimising inflammation following tissue injury.
 CC Sequence 481 AA;

Query Match 72.8%; Score 696; DB 5; Length 481;
 Best Local Similarity 75.0%; Pred. No. 1,37e-47;
 Matches 99; Conservative 16; Mismatches 12; Indels 5; Gaps 2;
 Db 25 qvqlv-qsgaevkpgssvkscasggtffsfyalswvraqpggglewmggiipifgtan 83
 QY 1 EVOLLEQSGAEVRKPGSSVKVSKASGGTFFSGHVTWVRQAPGGGLEWMGESIPFUSAN 60
 Db 84 yaq----kqgrvtitadeststamelsrsdttavvyrcardngaycggscysgwf 139
 QY 61 YAONYAQRFRDRVSIIDESTSTFIELSLRSDDTAVVYCYCARDPPRYCSAGRCYPGFFQ 120
 Db 140 pwqggtltvss 151
 QY 121 QWCGGTLTVSS 132

RESULT 2
 ID R54796 standard: peptide: 120 AA

AC R54796;
 DT 18-OCT-1994 (first entry)
 DE SPA-reactive IgM heavy chain clone KAS.
 KW SPA domain D; Ig binding region; IgM; B-cell superantigen; sAg;
 KW superantigen; heavy chain variable region; VH3 restricted antibody;
 KW VH: protein-A; KAS; B-lymphocyte; vaccine.
 OS Homo sapiens.
 PN WO9409818-A.
 PD 11-MAY-1994.
 PF 29-OCT-1993; U10555.
 PR 30-OCT-1992; US-969936
 PA (REGC) UNIV CALIFORNIA.
 PI Silverman GJ;
 DR WPI: 94-167127/20.
 PT Stimulating prodn. of variable region gene family restricted
 PT antibodies - through B-cell superantigen vaccination
 PS Disclosure: Page 78; 130pp; English.
 CC A B-cell superantigen (sAg) is a fragment of SPA D domain that
 CC specifically binds the Fab portion of variable region restricted
 CC antibodies. The sAg is used to enhance production of VH, especially
 CC VH3, restricted Abs. During attempts to identify sAgs, aa sequences
 CC (R54784-801) of H chains from Ig reactive with mod-SPA, and aa and
 CC DNA sequences (R54802-16, 064843-56) of VH regions of SPA binders
 CC obtained from combinatorial libraries were determined. IgM protein
 CC KAS is derived from the germline configuration of a VH gene
 CC segment.
 SQ Sequence 120 AA;

Query Match 58.5%; Score 559; DB 9; Length 120;
 Best Local Similarity 68.7%; Pred. No. 4.30e-36;
 Matches 90; Conservative 16; Mismatches 14; Indels 11; Gaps 7;

Db 1 vhlv-qsgaevkpgssvkscasggtffsfyalswvraqpggglewmggiipifg-q- 56
 QY 2 VOLLLEQSGAEVRKPGSSVKVSKASGGTFFSGHVTWVRQAPGGGLEWMGESIPFUSAN 61
 Db 57 a-nyackfggrvtitadeststamelsrsdttamycakeg--ygdygrpf-df--- 109
 QY 62 AONYAQRFRDRVSIIDESTSTFIELSLRSDDTAVVYCYCARDPPRYCSAGRCYPGFFQ 121
 Db 110 waqggtltvss 120
 QY 122 WCGGTLTVSS 132

RESULT 3
 ID R31023 standard: Protein: 476 AA.

AC R31023;
 DT 19-MAY-1993 (first entry)
 DE Antibody D heavy chain.
 KW Heavy: light; chain: antibody; D: monoclonal; peripheral; blood;
 KW lymphocyte; hepatitis A virus; HAV; sero: positive; patient; H.
 KW murine; B5B3; polyadenylated; cDNA library; human; Kappa; L; H.
 OS Synthetic.
 PN Synthetic.

Key Location/Qualifiers

FT Peptide 1..19
 FT /note= "Signal peptide"
 FT Region 20..49

FT /label= FR1
 FT Region 50..54

FT /label= CDR1
 FT Region 55..68

FT /label= FR2
 FT Region 69..84

FT /label= CDR2
 FT Region 85..113

FT /label= FR3
 FT Region 114..121

FT /label= CDR3
 FT Region 122..132

FT /label= FR4
 FT Domain 133..241

FT /label= CH1
 FT Region 242..262

FT /label= HINGE
 FT Domain 263..379

FT /label= CH2
 FT Domain 380..497

FT /label= CH3
 FT EP-523949-A.

PN 20-JAN-1993. 306420.

PD 14-JUL-1992; GB-015284.

PR 15-JUL-1991; GB-015284.

PR 01-AUG-1991; GB-015284.

PR 23-MAR-1992; GB-006284.

PA (WELL) WELLCOME FOUND LTD.

PI Crowe JS, Lewis AP;

DR WPI: 93-039951/03.

DR N-PSDB; Q35099.

PT Prod. of recombinant primate antibodies - useful for treating

PT infections caused by hepatitis A, B and C, herpes,

PT cytomegalovirus, AIDS, ARC, also treat multiple sclerosis,

PT arthritis etc.

PS Disclosure: Fig 2: 35pp; English.

CC The sequences given in R31023-24 represent the heavy and light chains

CC of Antibody D respectively. Antibody D is a monoclonal antibody which

CC was derived from peripheral blood lymphocytes from a hepatitis A virus

CC (HAV) sero positive patient. Antibody D is closely related in nature

CC to murine antibody B5B3. Total RNA was isolated from antibody D

CC expressing cells and polyadenylated RNA was extracted. These polyA

CC RNA's were used to prepare a cDNA library which was screened for human

CC kappa light (L) chains and two positive clones were detected.

CC Further heavy (H) chain clones were also isolated.

CC Sequence 476 AA;

SQ Query Match 58.3%; Score 557; DB 6; Length 476;

Best Local Similarity 64.4%; Pred. No. 6.32e-36;

Matches 85; Conservative 19; Mismatches 23; Indels 5; Gaps 3;

Db 20 qmqqv-qsgaevkpgssvkscasggtffsfyalswvraqpggglewmggiipifgt 78

QY 1 EVOLLEQSGAEVRKPGSSVKVSKASGGTFFSGHVTWVRQAPGGGLEWMGESIPFUSAN 60

Db 79 ysgnf-q---grvtitadeststamelsrsdttavvyrcardngaycggscysgwf 134

QY 61 YAONYAQRFRDRVSIIDESTSTFIELSLRSDDTAVVYCYCARDPPRYCSAGRCYPGFFQ 120

Db 135 pwqggtltvss 146

ID W1988 standard; Protein; 123 AA.

AC R72068

DI 26-SEP-1995 (first entry)

DE DP10 VH region

KW Graves ophthalmopathy associated immunoglobulin protein;

KW orbital antigen; monoclonal antibody; heavy chain; H chain;

KW variable region; autoimmunity.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1

FT /label= CDR2

FT /label= CDR3

PN WO9508336-A.

PD 30-MAR-1995.

PF 22-SEP-1994; U10756.

PR 22-SEP-1993; US-124469.

PA (NICH-) NICHOLS INST DIAGNOSTICS.

PI McLachlan SM, Rapoport B;

DR WPI: 95-139383/18.

DR N-PDB: Q89327.

PT Graves, ophthalmopathy-associated monoclonal antibody - produced by molecular cloning of immunoglobulin genes by PCR

PS Disclosure; Page 68; 94pp; English.

CC L- and H-chain DNA was amplified by PCR from Graves' orbital tissue and clones encoding autoimmune-associated immunoglobulin fragments were obtained. 13/15 clones of H chain (IgG) genes showed homology to the closest germ-line genes, D_HQ (Q89327) and CC h:1253 (Q89328). The DNA (Q89329) and corresp. amino acid sequence (R72070) sequences of the VH region of a representative clone, CC OFH1.2, are provided.

QC Sequence 98 AA:

SQ Query Match 55.0%. Score 537, EB 12. Length 98;
Best/Local Similarity 76.7%; Pred No. 2, 94e-34;
Matches 79; Conservative 13; Mismatches 6; Indels 5; Gaps

Db 1 qvqlv-qsgaevkpgsskvskasgdtfssyalswrtqapggglwmgsilpsftan 59
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Dy 1 EVQLLEQGSAEVRKPGSSVKVSKASGTFSCHVIITWRAPGVGLEWMGESIPFSSAN 60
:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
Db 60 yaq----kfqrvtideststymelsslrdsdttayyycaar 98
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 61 YAQNTAQAFPPFRVTIADSTSFIELSNLPDSHTAVYYCAAP 103
|||| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6

ID W19881 standard; Protein; 123 AA.

AC W19881;

DT 07-DEC-1997 (first entry)

DE CEA-specific antibody CEA6 VH sequence.

DW Carcinoembryonic antigen; CEA; Human; antibody; scPV;

KW tumour marker, lung cancer, breast cancer, colon cancer;

KW adenocarcinoma; diagnosis.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1

FT /note= "complementarity determining region 1"

FT Region 50..66

FT /label= CDR2

FT /note= "complementarity determining region 2"

FT Region 99..112

FT /label= CDR3

FT /note= "complementarity determining region 3"

PN WC9720932-Al.

PD 12-JUN-1997.

PF 09-DEC-1996. G03043.

PR 11-OCT-1996; GB-Q21295.

PR 27-DEC-1995; GB-Q25004.

PR 23-MAY-1996; GB-Q10824.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Allen DJ, McCafferty JG, Osbourn JK;

[illegible]

PT	non-cross-reactive with human liver cells; used for diagnosing
PT	Cancer
PT	Cancer
FS	Cancer
CC	Fig 2; 128pp; English.
CC	This polypeptide sequence comprises the heavy chain variable region
CC	(VH), HBB6, obtained by mutagenesis of the VH CDR3 of human
CC	carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
CC	W19881). A claimed specific binding member (A) comprises an hCEA
CC	specific antibody antigen binding domain that has a dissociation
CC	constant for hCEA of less than 1×10^{-8} M, is non-cross-reactive
CC	with human liver cells, and preferentially binds to the A3-B4
CC	extracellular domain of hCEA and/or to cell-associated hCEA over
CC	hCEA over soluble hCEA. Preferred (A) include pairings of VH and
CC	VL sequences from CEA3-7 (see W19676-85), or their CDR sequences,
CC	as well as CEA6 VH and VL variants (see W19886-95) obtained by
CC	mutagenesis or chain shuffling. An example of a claimed pairing
CC	is HBB6 VH with CEA6 VL. (A) is used to detect cells expressing
CC	hCEA, in vivo or in vitro, especially tumour cells for diagnosing
CC	cancer, e.g. adenocarcinoma of the colon, lung or breast.
CC	Sequence 123 AA;
CC	Query Match 55.88; Score 533; DR 23; Length 123;
CC	Best Local Similarity 65.94; Pred. No. 6,34e-34;
CC	Matches 87; Conservative 17; Mismatches 19; Indels 9; Gaps
Db	1 qvqlv-qsgaevkpgssvksckasqgltfnspsinwirqagqqlwmsuipstatan 59
QY	
QY	1 EVOLLNCSGAEPKPSKVVKVSKASGCTFSGHVITWVQAPVGGT FWMGESIP FGSAN 60
Db	60 yaq-----kfgrlritadeststymelssrdsctavvycaqrshly el-yyy-ymd 111
QY	
QY	61 YAQNYACKRFPDPSVIADESTSTSFTELSNRERSTAVVYVARGDPKYCAAGCTGFFPQ 120
Db	112 vwgggtmtvtyss 123
QY	
QY	121 QWCGGTLTVYSS 132
QY	
RESULT	8
IC	W19887 standard; Protein: 123 AA.
AD	W19887;
DE	07-DEC-1997 (first entry)
DE	CEA-specific antibody CEA6 VH mutant HBA11 sequence.
DE	Carcinoembryonic antigen; CEA; human; antibody; scfv;
KW	tumour marker; lung cancer; breast cancer; colon cancer;
KW	adenocarcinoma; diagnosis.
KW	adeno carcinoma; diagnosis.
OS	Chimeric Homo sapiens;
OS	Chimeric synthetic
Key	Location/Qualifiers
FT	Region 31...35
FT	/label= CDR1
FT	/note= "complementarity determining region 1"
FT	Region 50...66
FT	/label= CDR2
FT	/note= "complementarity determining region 2"
FT	Region 99...112
FT	/label= CDR3
FT	/note= "complementarity determining region 3"
FT	W09720932-A1.
PN	PN
PD	12-JUN-1997.
PP	09-DEC-1996; G03043.
PP	01-OCT-1996; GB-021295.
PP	07-DEC-1995; GB-025004.
PP	23-MAY-1996; GB-010824.
PA	(CAAB-) CAMPRIDGE ANTIBODY TECHNOLOGY.
PA	Allen NJ, McCafferty JC, Osbourn JW;
PT	WPI; 97-319779/29.
PT	Specific binding members for human carcinoembryonic antigen - bind
PT	to the A3-B4 extracellular domain of hCEA and are substantially
PT	non-cross-reactive with human liver cells; used for diagnosing
PT	Cancer
PT	Cancer
FS	Cancer
CC	Fig 2; 128pp; English.
CC	This polypeptide sequence comprises the heavy chain variable region
CC	(VH), HBA11, obtained by mutagenesis of the VH CDR3 of human

hCEA over soluble hCEA. Preferred (A) include pairings of VH and VL sequences from CEA1-7 (see W19876-85), or their CDP sequences, as well as CPA6 VH and VL variants (see W1986-95) obtained by mutagenesis or chain shuffling. Examples of claimed pairings are TCSC10 VH with TCSP12 or CEA5 VL. (A) is used to detect cells expressing hCEA, *in vivo* or *in vitro*, especially tumour cells for diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast. Sequence 123 AA;

Query Match	55.4%	Score 530;	DB 23;	Length 123;
Best Local Similarity	65.9%;	Pred. No. 1.13e-33;		
Matches	87;	Conservative	17;	Mismatches 19;
				Indels 9;
				Gaps 5;

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Db      1 qvqlv-qsgaevkpssvkckasqgtfsnplwlrqagggilewmsiipstfatn 59
      |||||
      1 EVTLLESGSAEVRKPSVAVKSTKASGRIFSHVITWVLPAPGSLLEWMEFIPFISAN 60
      |||||
Db      60 yaq----kfgritlatadestatymelsslrtsodtavycageshy-cl-yyy---ymd 111
      |||||
      61 YAQNYAKFEDRVYSIIADESTSTSFIEUNLSDLDIAVYCARGFPRYCAGKCYCFGFQ 120
      |||||
Db      112 vwgggmtvtvss 123
      |||||
      121 CWGGSILVTVSS 132
      |||||

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112 vwgqgtmvtvss 123
      | | | | |
121 OWGOGILVTVSS 132

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RESULT 10
ID R65019 standard: Protein: 147 AA.

DE 02-OCT-1995 (first entry)
DF 93XAG anti-Varicella zoster virus antibody heavy chain variable.
DE region.
DE Varicella zoster virus: VZV, anti-VZV monoclonal antibody, 93PA9
KW Varicella zoster virus: VZV, anti-VZV monoclonal antibody, 93PA9
KW glycoprotein II subunit; vaccine.
OS Synthetic.

Key	Location/Qualifiers
FT	20..147
FT	protein= mature light chain
FT	Region 50..54
FT	/label= complementarity determining region (CDR) region 60..85

FT	/label= CDR	118..136
FT	Region	
FT	/label= CDR	
PN	WQ9504D80-A.	
PD	09-FEB-1995.	
FE	22-JUL-1994.	U09241..
FE	28-JUL-1993.	US-098479.
FE	24-MAR-1994.	US-217918.
PA	(SANO) SANDOZ PHARM CORP.	
PI	Lake P. Ostberg L.	
DP	WF1: 95-090612/12.	
DP	N-PSDB; Q82750.	
DPT	Human monoclonal antibodies specific for the glyco:protein II	
FE	subunit of varicella zoster virus . used in a therapy and	
FE	prophylaxis of infection	
PT	Claim 8; Fig 4B; 39pp; English.	

A human anti-Varicella zoster virus monoclonal antibody was prepared using the ELISA method of Gershon et al. (1983) where IgG₁, IgG₂, IgM, one resultant plasma cell fused v.v. in the absence of centrifugation. This cell line designated cell line TCSKAg produced an antibody designated oAkAg cDNA for the light and heavy chain variable region genes of the oAkAg antibody were cloned using PCR at least two heavy chain (gamma-1 and two light chain kappa) specific clones were sequenced (ssg 082749 & 082750 respectively).

Db 20 qvqlv-qsgaevkpgssvkvsckasggtfsnfaiswrvqpggglegwmgrimplfts-77

QY 1 EVOLLEQSGAEVKKPSSVKVSCKASGTSFSGHIVTWRQAPGQGLEWMGESIPIFGSAN 60
 Db 78 -t--yqkfggrvtisadastaymelslrsddtdamvycardita-pgaaptplniyg 133
 QY 61 YAUHYAKKFPKPVSIADGSTSFISFLSNLSGHTAVYVCAKAPKPYASAGPYVAF- 119

Db 134 mdvvgggtttvss 147
 QY 120 QQ-WGQGLTVTVSS 132

RESULT 11
 ID W13536 standard; protein: 119 AA.

AC W13536;
 DT 28-OCT-1997 (first entry)
 DE Anti-melanoma antibody 2-71 from VH antibody fusion phage library.
 KW Human: monoclonal antitumor antibody; peripheral blood lymphocyte.
 KW cancer: tumorigenesis; anticancer vaccine.
 OS Homo sapiens.
 PN MO9702479-A2.
 PD 23-JAN-1997
 PF 28-JUN-1996; IB1032.
 PR 30-JUN-1995; US-497647.
 PA (UYVA) UNIV VALE.
 PI Cai X, Garen A.
 WPI: 97-109061/10.

PT Prodn. of human monoclonal anti-tumour antibodies - by screening a
 PT fusion phage library produced using peripheral blood lymphocytes
 PT from a cancer patient
 PS Claim 19; Page 75:76; 82pp; English.
 CC A process for isolating and synthesising human monoclonal anti-tumour
 CC antibodies has been produced. The process involves: (a) constructing at
 CC least one fusion phage library from the peripheral blood lymphocytes at
 CC (PBUs) of a cancer patient; (b) screening for anti-tumour antibodies in
 CC the phage library in a binding assay with cultured tumour cells of the
 CC same type as the patient's tumour; (c) removing extraneous antibodies by
 CC absorption against normal human cells; (d) cloning the phage selected in
 CC step (b) and (c); (e) assaying the specificity of the cloned phage by
 CC incubating the phage with at least two types of cultured normal cells;
 CC and (f) further testing the specificity of cloned phage that do not bind
 CC to either cell line of cultured normal cells in further binding assays
 CC to cultured tumour cells derived from more than one other tumour that is
 CC not the patient's tumour. The present sequence represents a human heavy
 CC chain antibody, from a VH antibody fusion phage library, produced by
 CC a method as described above. The antibodies produced can be used for
 CC diagnostic and therapeutic applications and for isolating tumour
 CC antigens for studying tumourigenesis or for use as anti-cancer vaccines.
 CC The human antibodies have low immunogenicity in humans compared to
 CC murine monoclonal antibodies (MABs). Since the antibodies are isolated
 CC from fusion phage libraries, their affinity and specificity for a
 CC tumour cell line can be improved by genetic manipulations.
 SQ Sequence 119 AA;

Query Match 55.0%; Score 526; DB 23; Length 119.
 Best Local Similarity 69.6%; Pred. No 2 43e-33;
 Matches 87; Conservative 16; Mismatches 10; Indels 12; Gaps 4;

Db 7 gglevkkpssvkvscasggtfssyaiswvrgqgglewmgglipifqtanyaq---- 62
 QY 8 SGAEVKPSSVKVSKASGGIFSGHIVTWRQAPGQGLEWMGESIPIFGSANYAQNVAQ 67
 Db 63 kfggrvtitadkststamelslrsdstavvyicar-----qgar-ydaf-diwgqatl 114
 QY 68 KFPDRVSIADGSTSFISFLSNLSGHTAVYVCAKAPKPYASAGPYVAFQWQGITL 127
 Db 115 vtvs 119
 QY 128 VTVSS 132

RESULT 12
 ID R45610 standard; Protein: 124 AA.
 AC R45610;

DT 22-JUL-1994 (first entry)
 DE Monoclonal antibody GP68 heavy chain (V H 1).
 KW HIV: Human Immunodeficiency Virus; gp120; glycoprotein;
 KW envelope protein, monoclonal antibody. MAH: vaccine; therapy.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 31..35
 FT /label= CDR 1
 FT Region 50..66
 FT /label= CDR 2.
 FT Region 99..110
 FT /label= CDR 3.
 FT Region 111..124
 FT /label= Framework IV, JH4 segment.
 PN EP-581353-A.
 PD 02-FEB-1994.
 PF 05-JUL-1993; 201959.
 PR 03-JUL-1992; EP-202032.
 PA (NEWB-) NEDERLANDEN. MIN WELZIJN.
 PI Osterhaus ADME:
 WPI: 94-036603/05.
 IN N-PSDB: Q55663.
 PT Monoclonal antibodies to HIV-1 - directed against glyco:protein
 PT gp120, useful for passive immunotherapy or prodn. of
 PT anti-idiotype vaccines
 PS Claim 6; Page 22-23; 34pp; English.
 CC The monoclonal antibodies (MAB's) designated GP13, GP44 and GP68
 CC react with HIV-1 gp120 glycoprotein variants containing the amino
 CC acids Asn88, Lys117, Asn262 and Tyr 435 but exhibit at least 50%
 CC reduced reaction with gp120 variants in which these amino acids
 CC have been deleted or substituted. The MAB's are useful for passive
 CC immunotherapy and their anti-idiotype antibodies can be used in the
 CC production of vaccines.
 SQ Sequence 124 AA;

Query Match 54.5%; Score 521; DB 9; Length 124;
 Best Local Similarity 62.9%; Pred. No. 6 32e-33;
 Matches 83; Conservative 19; Mismatches 22; Indels 8; Gaps 6;

Db 1 qqlv-qsgaevkpkssvkvscasggtfssstlhwvrgtqgqglwmmkiiptlgsst 59
 QY 1 EVOLLEQSGAEVKKPSSVKVSCKASGTSFSGHIVTWRQAPGQGLEWMGESIPIFGSAN 60
 Db 60 yspffq---grvltladeststvmelslrsdstavvyckasgqswslirs-p-aid 112
 QY 61 YAUHYAKKFPKPVSIADGSTSFISFLSNLSGHTAVYVCAKAPKPYASAGPYVAF- 119
 Db 113 nwdgggtltvss 124
 QY 121 QWGGTILTVSS 132

RESULT 13
 ID P72063 standard; Protein: 98 AA.

AC P72063;
 DT 26-SEP-1995 (first entry)
 DE HV1263 VH region.
 KW Graves ophthalmopathy associated immunoglobulin protein;
 KW orbital antigen; monoclonal antibody; heavy chain; H chain;
 KW variable region; autoimmunity.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Region 31..35
 FT /label= CDR1
 FT Region 50..66
 FT /label= CDR2
 PN W09508336-A.
 PD 30-MAR-1995.
 PF 22-SEP-1994; U10756.
 PR 22-SEP-1993; US-124469.
 PA (NICH-) NICHOLS INST DIAGNOSTICS.
 PI McLachlan SM. Rapoport B;
 WPI: 95-139383/18.

DR N-PSDB; Q89328.
 PT Graves' ophthalmopathy-associated monoclonal antibody - produced
 PT by molecular cloning of immunoglobulin genes by PCR
 PS Disclosure: Page 69; 94pp; English.
 CC L- and H-chain DNA was amplified by PCR from Graves' orbital
 CC tissue and clones encoding autoimmune-associated immunoglobulin
 CC fragments were obtained. 13/15 clones of H chain (IgG1) genes
 CC showed homology to the closest germline genes, DP10 (Q89327) and
 CC hV1262 (Q89328). The DNA (Q89329) and corresp. amino acid
 CC (R72070) sequences of the VH region of a representative clone.
 CC QF7H1.2, are provided.
 SQ Sequence 98 AA;

Query Match 53.9%; Score 515; DB 12; Length 98;
 Best Local Similarity 74.8%; Pred. NO. 2,00e-32;
 Matches 77; Conservative 13; Mismatches 8; Indels 5; Gaps 4;

Db 1 qvqlv-qsgaevkpgssvkvsckasggtffssyaiswvrqapggglewmgrilp-i- 57
 QY 1 EVULLQSGAEVFKPKPSSVKVSKASGGTFSSHVITWVFPQAPQVLEWMSPIPIFSSAN 60

Db 58 -a-nyackkfgrvtitadkstststymelsslrscdtavyycaar 98
 QY 61 YACNYACKFPDPVSIADSTSTSFTEISNLPSSDTAVVYCAP 103

RESULT 14
 ID R22358 standard; Protein: 117 AA.

AC R22358;
 DT 17-AUG-1992 (first entry)
 DE Protein encoded by the human heavy chain V region gene VH49.8.
 KW Heavy chain: variable region; VH1 family.
 OS Homo sapiens.
 PN WC9203918-A.
 PD 19-MAR-1992.
 PE 28-AUG-1991; U06185.
 PF 29-AUG-1990; Y5-574748.
 PR 31-AUG-1990; Y5-575062
 PA (GENP-) GENPHARM INT INC
 PI Lonberg N. Kay R;
 DR WPI: 92-113062/14.
 DP N-PSDB: Q22419
 PT Immunoglobulin transgenes - for prodn. of heterologous
 PT non-rearranged and/or rearranged Ig chains
 PS Example 14; Page 87; 172pp; English.
 CC The human placental genomic DNA library cloned into the phage
 CC vector lambda FIX II was screened with the human VH1 family
 CC specific oligonucleotide (see Q22418). Phage clone lambda
 CC 49.8 was isolated and a 6.1 kb XbaI fragment contg. the variable
 CC segment VH49.8 subcloned into pNN03 to generate plasmid pVH49.8.
 CC An 800 bp region of this insert was sequenced. VH49.8 was found
 CC to have an open reading frame which encoded the sequence shown..
 SQ Sequence 117 AA;

Query Match 53.9%; Score 515; DB 4; Length 117;
 Best Local Similarity 74.8%; Pred. NO. 2,00e-32;
 Matches 77; Conservative 13; Mismatches 8; Indels 5; Gaps 4;

Db 20 qvqlv-qsgaevkpgssvkvsckasggtffssyaiswvrqapggglewmgrilp-i- 76
 QY 1 EVULLQSGAEVFKPKPSSVKVSKASGGTFSSHVITWVFPQAPQVLEWMSPIPIFSSAN 60

Db 77 -a-nyackkfgrvtitadkstststymelsslrscdtavyycaar 117
 QY 61 YACNYACKFPDPVSIADSTSTSFTEISNLPSSDTAVVYCAP 103

RESULT 15
 ID R38623 standard; Protein: 117 AA.

AC R38623;
 DT 10-NOV-1993 (first entry)
 DE Human heavy chain V region VH49.8.
 KW Immunoglobulin; IgG; heavy chain; minilocus transgene;

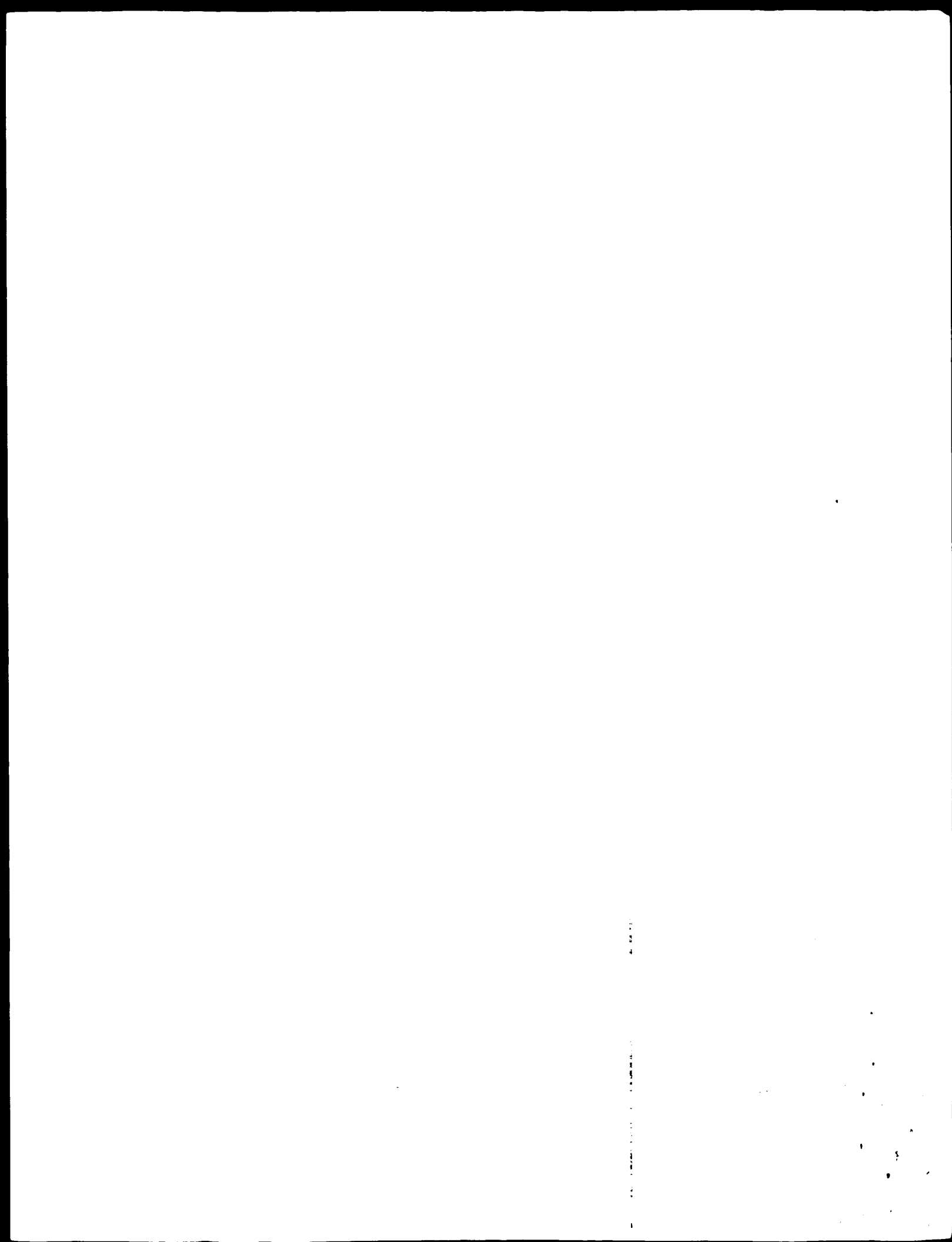
KW isotype switching; H chain variable region.
 OS Homo sapiens.
 PN WC931227-A.
 PD 24-JUN-1993.
 PE 17-DEC-1992; U10983.
 PF 17-DEC-1991; US-810279.
 PR 18-MAR-1992; US-853408.
 PP 23-JUN-1992; US-904068.
 PA (GENP-) GENPHARM INT INC.
 PI Kay RM, Lonberg N;
 DR WPI: 93-214169/26.
 DP N-PSDB: Q44185.
 PT Transgenic non-human animals contg. immunoglobulin heavy chain
 PT transgene - used to produce useful antibodies by isotype
 PT switching
 PS Example 12, Page 96; 196pp; English.
 CC A human placental genomic DNA library cloned into the phage vector
 CC lambda FIX II was screened with the human VH1 family specific
 CC oligonucleotide Q44184. Phage clone lambda 49.8 was isolated and a
 CC 6.1 kb XbaI fragment containing the variable segment VH49.8 was
 CC subcloned into pNN03 to generate plasmid pVH49.8. An 800bp
 CC region of this insert was sequenced (Q44185) and VH49.8 found to
 CC have an open reading frame and intact splicing and recombination
 CC signals, indicating that the gene is functional. Amino acid
 CC sequence Q44185 was deduced from the coding sequence; the last 3
 CC codons before the termination codon have not been translated.
 SQ Sequence 117 AA;

Query Match 53.9%; Score 515; DB 7; Length 117;
 Best Local Similarity 74.8%; Pred. NO. 2,00e-32;
 Matches 77; Conservative 13; Mismatches 8; Indels 5; Gaps 4;

Db 20 qvqlv-qsgaevkpgssvkvsckasggtffssyaiswvrqapggglewmgrilp-i- 76
 QY 1 EVULLQSGAEVFKPKPSSVKVSKASGGTFSSHVITWVFPQAPQVLEWMSPIPIFSSAN 60

Db 77 -a-nyackkfgrvtitadkstststymelsslrscdtavyycaar 117
 QY 61 YACNYACKFPDPVSIADSTSTSFTEISNLPSSDTAVVYCAP 103

Search completed: Tue Feb 24 07:03:57 1998
 Job time : 41 secs.



MORFAL

(1M)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run on: Tue Feb 24 07:31:49 1998: MasPar time 3.19 Seconds
210,908 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-1
Description: (1-132) from US08844215.pep
Perfect Score: 956
Sequence: 1 EVQLLESGAEVRKPGSSVK PCYPGFFQNGGTLTVSS 132

Scoring table: PAM 150
Gap 11

Searched: 56402 seqs, 5095871 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued
1:Back1 2:51 3:52 4:53 5:54 6:55 7:56 8:57 9:58 10:59
10:PCP92 11:PCP93 12:PCP94 13:PCP95 14:PCP96

Statistics: Mean 28.605 Variance 140.983 scale 0.203

Pred No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	607	63.5	129.13	PCT-US95-0	Sequence 45, Application	2.43e-41
2	559	58.5	120.11	PCT-US93-1	Sequence 13, Application	2.79e-37
3	539	56.4	120.11	PCT-US93-1	Sequence 12, Application	1.36e-35
4	529	55.3	147.6	US-08-477	Sequence 47, Application	9.44e-33
5	515	53.9	102.10	PCT-US92-0	Sequence 65, Application	1.42e-29
6	515	53.9	102.10	PCT-US92-0	Sequence 63, Application	1.42e-29
7	515	53.9	102.7	US-07-634	Sequence 55, Application	1.42e-29
8	515	53.9	102.7	US-08-053	Sequence 63, Application	1.42e-29
9	515	53.9	122.12	PCT-US95-0	Sequence 3, Application	1.42e-29
10	512	53.6	121.11	PCT-US93-1	Sequence 8, Application	2.54e-33
11	512	53.6	140.11	PCT-US93-1	Sequence 12, Application	2.54e-33
12	489	51.2	117.6	US-08-477	Sequence 4, Application	2.17e-31
13	489	51.2	117.6	US-08-477	Sequence 15, Application	2.17e-31
14	489	51.2	117.6	US-07-634	Sequence 15, Application	2.17e-31
15	489	51.2	117.6	US-07-634	Sequence 72, Application	2.17e-31
16	489	51.2	117.6	US-08-477	Sequence 14, Application	2.17e-31
17	489	51.2	117.6	US-07-634	Sequence 4, Application	2.17e-31
18	489	51.2	117.6	US-08-477	Sequence 72, Application	2.17e-31
19	489	51.2	117.7	US-08-474	Sequence 104, Application	2.17e-31
20	489	51.2	117.7	US-08-474	Sequence 15, Application	2.17e-31
21	489	51.2	117.7	US-08-474	Sequence 4, Application	2.17e-31
22	489	51.2	117.7	US-08-474	Sequence 4, Application	2.17e-31

23	489	51.2	117.7	US-08-487	Sequence 15, Application	2.17e-31
24	489	51.2	117.7	US-09-474	Sequence 72, Application	2.17e-31
25	489	51.2	117.7	US-08-487	Sequence 104, Application	2.17e-31
26	489	51.2	117.7	US-08-487	Sequence 72, Application	2.17e-31
27	489	51.2	117.6	US-07-634	Sequence 104, Application	2.17e-31
28	481	50.3	121.6	US-07-634	Sequence 53, Application	1.03e-30
29	481	50.3	121.7	US-08-487	Sequence 53, Application	1.03e-30
30	481	50.3	121.7	US-08-474	Sequence 53, Application	1.03e-30
31	481	50.3	121.6	US-08-477	Sequence 53, Application	1.03e-30
32	476	49.8	116.6	US-08-487	Sequence 6, Application	2.67e-30
33	476	49.8	116.6	US-07-634	Sequence 6, Application	2.67e-30
34	476	49.8	116.6	US-08-477	Sequence 6, Application	2.67e-30
35	476	49.8	116.6	US-08-474	Sequence 6, Application	2.67e-30
36	476	49.8	140.6	US-07-945	Sequence 28, Application	2.67e-30
37	472	49.4	124.7	US-04-478	Sequence 63, Application	2.67e-30
38	471	49.3	123.13	PCT-US95-0	Sequence 11, Application	7.05e-40
39	471	49.3	142.13	PCT-US93-1	Sequence 17, Application	7.05e-40
40	468	49.0	117.11	PCT-US93-1	Sequence 7, Application	1.25e-29
41	468	49.0	119.13	PCT-US95-0	Sequence 12, Application	1.25e-29
42	465	48.5	119.13	PCT-US95-0	Sequence 10, Application	2.23e-29
43	462	48.3	116.6	US-07-634	Sequence 5, Application	3.97e-29
44	462	48.3	116.6	US-08-477	Sequence 5, Application	3.97e-29
45	462	48.3	135.6	US-07-634	Sequence 19, Application	3.97e-29

ALIGNMENTS

RESULT 1
ID PCT-US95-01219-45 STANDARD: PPT: 129 AA.
XX
AC xxxxxx
XX
DT 01-JAN-1900
XX
DE Sequence 45, Application PC/TUS9501219.
DE
XX Sequence 45, Application PC/TUS9501219
CC
CC Sequence 45, Application PC/TUS9501219
CC GENERAL INFORMATION:
CC APPLICANT: Bendly, Mary M.
CC APPLICANT: Legier, Olivier J.
CC APPLICANT: Saidanah, Jose
CC APPLICANT: Jones, S. Tarran
CC TITLE OF INVENTION: Humanized Antibodies Against Leptocyte
CC TITLE OF INVENTION: Adhesion Molecule VLA-4
CC NUMBER OF SEQUENCES: 45
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Townsend and Townsend Khourie and Crew
CC STREET: One Market Plaza, Steuart Tower, Suite 2000
CC CITY: San Francisco
CC STATE: California
CC COUNTRY: USA
CC ZIP: 94105
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC Compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent Release #1.0, Version #1.03
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US95/01219
CC FILING DATE: 25-JAN-1995
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/126,269
CC FILING DATE: 25-JAN-1994
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Smith, William L.
CC REGISTRATION NUMBER: 30,223
CC REFERENCE/DOCCT NUMBER: 15270-14
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 415-543-9600
CC TELEFAX: 415-543-5043
CC INFORMATION FOR SEQ ID NO: 45:
CC SEQUENCE CHARACTERISTICS:

```

CC LENGTH: 129 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 129 AA: 13930 MW: 96169 CN:

Query Match 63.5%; Score 607, DB 13; Length 129;
Best Local Similarity 67.2%; Pred. No. 2,43e-41;
Matches 90; Conservative 22; Mismatches 15; Indels 7; Gaps 7;

Db 1 QVOLV-OSGAEVKPKGASVVKVCKASGYTFTSYAISWVRQAPGQGLEWVG-WINPYGND 58
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVOLLEQSGAEVKKPGSSVVKVCKASGTFSGHVITWVRQAPGQGLEWVGSIPIFGSAN 60

Db 59 -T-NYAKQFQGRVITADTSTSTAYMELSLRSDETVAVYCARAPG-VGSGGGCYRGDYX 115
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 YAQNYAKFRDVRVSIADSTSTSIELSLNLRSDDTAVYCYCARDPPRYCSAGRCYPG-F 118

Db 116 FDYWGQGLTVTVSS 129
QY :|||||:|||||:
119 FQWGGQGLTVTVSS 132

RESULT 2
ID PCT-US93-10555-13 STANDARD: PRT: 120 AA.
XX xxxxxx
XX AC
XX AC
XX 01-JAN-1900
XX
XX Sequence 13, Application PC/TUS9310555.
XX
XX Sequence 13, Application PC/TUS9310555
CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
CC THROUGH
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
CC ATES
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM.
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: FD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 13:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 120 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide

IMMEDIATE SOURCE:
CC CLONE: KAS
CC FEATURE:
CC NAME/KEY: Peptide
CC LOCATION: 1-120
CC SEQUENCE 120 AA: 13008 MW: 78865 CN:

Query Match 58.5%; Score 550, DR 11; Length 120;
Best Local Similarity 68.7%; Pred. No. 2,79e-37;
Matches 90; Conservative 16; Mismatches 14; Indels 11; Gaps 7;

Db 1 VHLV-OSGAEVKPKGSSVVKVCKASGTFSSVAISWVRQAPGQGLEWVGSIPIFG--Q 56
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 VOLLESGAEVKKPGSSVVKVCKASGTFSGHVITWVRQAPGQGLEWVFSIPIFGSANY 61

Db 57 A-NYAKQFQGRVITADSTNTAYMELSLRSDDTAMVYCAKPG--YDYGKPF-IF--- 109
QY :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 AQNYAKFRDVRVSIADSTSTSIELSLNLRSDDTAVYCYCARDPPRYCSAGRCYPGFFQ 121

Db 110 WGGQGLTVTVSS 120
QY :|||||:|||||:
122 WGGQGLTVTVSS 132

RESULT 3
ID PCT-US93-10555-12 STANDARD: PRT: 120 AA.
XX xxxxxx
XX AC
XX AC
XX 01-JAN-1900
XX
XX Sequence 12, Application PC/TUS9310555.
XX
XX Sequence 12, Application PC/TUS9310555
CC GENERAL INFORMATION:
CC APPLICANT: SILVERMAN, GREGG J.
CC TITLE OF INVENTION: METHOD FOR STIMULATING PRODUCTION OF
CC TITLE OF INVENTION: VARIABLE REGION GENE FAMILY RESTRICTED ANTIBODIES
CC THROUGH
CC TITLE OF INVENTION: VACCINATION WITH A B-CELL SUPERANTIGEN AND CONJUG
CC ATES
CC TITLE OF INVENTION: THEREOF
CC NUMBER OF SEQUENCES: 51
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Spensley Horn Jubas & Lubitz
CC STREET: 1880 Century Park East - Suite 500
CC CITY: Los Angeles
CC STATE: California
CC COUNTRY: USA
CC ZIP: 90067
CC COMPUTER READABLE FORM.
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: PCT/US93/10555
CC FILING DATE: 29-OCT-1993
CC CLASSIFICATION:
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Howells, Stacy L.
CC REGISTRATION NUMBER: 34,842
CC REFERENCE/DOCKET NUMBER: FD-2630
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (619) 455-5100
CC TELEFAX: (619) 455-5110
CC INFORMATION FOR SEQ ID NO: 12:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 120 amino acids
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: linear
CC MOLECULE TYPE: peptide

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CC IMMEDIATE SOURCE:
CC CLONE: BOR
CC FEATURE:
CC NAME/KEY: Peptide-
CC LOCATION: 1-120
CC SEQUENCE 120 AA: 12984 MW: 80845 CN:

Query Match 56.4%: Score 530; DP 11; Length 120;
Best Local Similarity 56.4%; Prod No. 136e-35;
Matches 87; Conservative 20; Mismatches 13; Indels 11; Gaps 5:

Db 1 VOLV-OSGAEVKPKGSSVAVTKASDTFSSAISWVROAPQGGLEWGGIPIPGTNY 59
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 2 VOLV-OSGAEVKPKGSSVAVTKASDTFSSAISWVROAPQGGLEWGGIPIPGTNY 51
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 60 AQ-----KFGPVTITTDRTSTAYMVSLSRSDTALYYCAPEGPPM-AIN---P--FDY 109
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 AQNYAKFFPVPVSIADSTISFISLSNLSRSDTAVVYCAPEGPPYVSAGRCYGFQQ 121
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 110 WGGGTLTVSS 120
QY 122 WGGGTLTVSS 132

RESULT 4
ID US-08-217-918-4 STANDARD: PRT: 147 AA
XX AC xxxxxx
XX DT 01-JAN-1900
XX DE
XX SE
XX SEQUENCE 4, Application US/08217918.
XX
XX SEQUENCE 4, Application US/08217918
XX Patent No. 5506132
XX GENERAL INFORMATION:
XX APPLICANT: LAKE, PHILIP
XX APPLICANT: OSTBERG, LARS
XX TITLE OF INVENTION: HUMAN ANTIBODIES AGAINST
XX TITLE OF INVENTION: VARICELLA-ZOSTER VIRUS
XX NUMBER OF SEQUENCES: 4
XX CORRESPONDENCE ADDRESS:
XX ADDRESS: Townsend and Townsend Kheourie and Crew
XX STREET: 379 Lytton Avenue
XX CITY: Palo Alto
XX STATE: California
XX COUNTRY: US
XX ZIP: 94301
XX COMPUTER READABLE FORM:
XX MEDIUM TYPE: Floppy disk
XX COMPUTER: IBM PC compatible
XX OPERATING SYSTEM: PC-DOS/MS-DOS
XX SOFTWARE: Patent In Release #1.0, Version #1.25
XX CURRENT APPLICATION DATA:
XX APPLICATION NUMBER: US/08/217 918
XX FILING DATE: 24-MAR-1994
XX CLASSIFICATION: 530
XX ATTORNEY/AGENT INFORMATION:
XX NAME: Smith, William M
XX REGISTRATION NUMBER: 30,223
XX TELECOMMUNICATION INFORMATION:
XX TELEPHONE: (415) 326-2400
XX TELEFAX: (415) 326-2422
XX INFORMATION FOR SEQ ID NO: 4:
XX SEQUENCE CHARACTERISTICS:
XX LENGTH: 147 amino acids
XX TYPE: amino acid
XX TOPOLOGY: linear
XX MOLECULE TYPE: protein
XX SEQUENCE 147 AA: 15801 MW: 123306 CN:

Query Match 55.3%: Score 520; DP 6; Length 147;
Best Local Similarity 54.2%; Prod No. 9 44e-25;
Matches 77; Conservative 13; Mismatches 8; Indels 5; Gaps 4;

Db 5 QVOLV-OSGAEVKPKGSSVAVTKASDTFSSAISWVROAPQGGLEWGGIPIPGTNY 61
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 EVOLV-OSGAEVKPKGSSVAVTKASDTFSSAISWVROAPQGGLEWGGIPIPGTNY 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 52 -A-NYAKFGPVTITTDRTSTAYMVSLSRSDTAVVYCAPEGPPYVSAGRCYGFQQ 102
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```


US-08-844-215-1.rai

Thu Feb 26 07:03:34 1998

APPLICATION NUMBER: PCT/US93/11612

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION NUMBER: US 07/983,946

FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 121 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 121 AA: 13661 MW: 87993 CN;

Query Match 53.6%; Score 512; DB 11; Length 121;

Best Local Similarity 61.4%; Pred. No. 2,54e-33;

Matches 81; Conservative 24; Mismatches 16; Indels 11; Gaps 7;

Db 1 QVQLV-QSGAEVKKFGSSVKVSKASGYTFTSYVMHVRQAPGGGLEWIG--Y-IYFVND 56

QY 1 EVQLLEQSGAEVRRKPGSSVKVSKASGGTFTSGHVTITVWRQAPGGGLEWIGESIPFGSAN 60

Db 57 -GTKYNEKFGKRVITTSDESTINAYMELSSLRSEDATVYYCAREE--Y--GN-YVRYEV 109

QY 61 YAQNYAQKFRDVSITIADESTSTFIELSNLRSDDTAVYYCARDPPRYCSAGRCYPGFFQ 120

Db 110 DWGGTGLTVSS 121

QY 121 QWGGTGLTVSS 132

RESULT 11

ID PCT-US93-11612-12 STANDARD: PRT: 140 AA

XX xxxxxx

DT 01-JAN-1900

Sequence 12, Application PC/TUS9311612.

Sequence 12, Application PC/TUS9311612

GENERAL INFORMATION:

APPLICANT: Co. Man Supg

TITLE OF INVENTION: Humanized Antibodies Reactive with

TITLE OF INVENTION: L-Selectin

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Khourie and Crew

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/11612

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION NUMBER: US 07/983,946

FILING DATE: 01-DEC-1992

ATTORNEY/AGENT INFORMATION:

NAME: Smith, William M.

REGISTRATION NUMBER: 30,223

REFERENCE/DOCKET NUMBER: 11823-22

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-326-2400

TELEFAX: 415-326-2422

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 140 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 140 AA: 15650 MW: 117746 CN;

Query Match 53.6%; Score 512; DB 11; Length 140;

Best Local Similarity 61.4%; Pred. No. 2,54e-33;

Matches 81; Conservative 24; Mismatches 16; Indels 11; Gaps 7;

Db 20 QVQLV-QSGAEVKKFGSSVKVSKASGYTFTSYVMHVRQAPGGGLEWIG--Y-IYFVND 75

QY 1 EVQLLEQSGAEVRRKPGSSVKVSKASGGTFTSGHVTITVWRQAPGGGLEWIGESIPFGSAN 60

Db 76 -GTKYNEKFGKRVITTSDESTINAYMELSSLRSEDATVYYCAREE--Y--GN-YVRYEV 128

QY 61 YAQNYAQKFRDVSITIADESTSTFIELSNLRSDDTAVYYCARDPPRYCSAGRCYPGFFQ 120

Db 129 VWGGTGLTVSS 140

QY 121 QWGGTGLTVSS 132

RESULT 12

ID US-08-477-728-4 STANDARD: PRT: 117 AA

XX xxxxxx

DT 01-JAN-1900

Sequence 4, Application US/08477728.

Sequence 4, Application US/08477728

GENERAL INFORMATION:

APPLICANT: QUEEN, Cary L.

APPLICANT: SCHNEIDER, William P.

APPLICANT: SELICK, Harold E.

TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS

NUMBER OF SEQUENCES: 113

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: Palo Alto

STATE: California

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/477,728

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/634,278

FILING DATE: 19-DEC-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/418,252

MORFEL
(TX)

Release 2.1D John F. Collins, Biocomputing Research Unit
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:03:36 1998. Master file: R.F. Smith
Tabular output not generated
Title: >US-08-844-215-1
Description: (1-132) from US08844215.pcp
Perfect Score: 956
Sequence: 1 EVQLLEQSGAEVPRKPGSSVK... PCYPGFPQWGGTLTVSS 132

Scoring table: PAM 150
Gap 11
Searched: 95051 seqs, 30469580 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries
Database: p1r53
1:ann1 2:ann2 3:ann3 4:ann4 5:annn1 6:unann2 7:unann3
8:unann4 9:unann5 10:unann6 11:unann7 12:unann8
13:unann9 14:unann10 15:unann11 16:unann12 17:unann
18:unrev

Statistics: Mean 41.620; Variance 105.958; scale 0.393
Pred No is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES				
Result No.	Score	Query Match	Length DP ID	Description
1	632	66.1	126	Ig heavy chain V reg 3.49e-64
2	594	61.1	128	Ig heavy chain V reg 3.49e-64
3	579	60.6	128	Ig heavy chain V-1 reg 7.23e-64
4	577	60.4	127	Ig heavy chain V-1 reg 7.23e-64
5	575	60.1	126	Ig heavy chain V-1 reg 7.23e-64
6	567	59.3	160	anti-PR2 erythrocyte 6.10e-69
7	566	59.2	120	Ig heavy chain V-1 reg 8.80e-69
8	560	58.6	135	Ig heavy chain V-1 reg 7.90e-68
9	559	58.5	137	Ig heavy chain V-1 reg 1.14e-67
10	551	57.6	129	Ig heavy chain V reg 2.11e-66
11	549	57.4	116	Ig heavy chain V reg 4.39e-66
12	545	57.1	121	Ig heavy chain V reg 1.31e-65
13	545	57.1	132	Ig heavy chain V reg 1.31e-65
14	545	57.0	133	Ig heavy chain V-1 reg 1.89e-65
15	545	57.0	627	Ig mu chain precursor 1.89e-65
16	544	56.9	126	Ig heavy chain V reg 2.72e-65
17	542	56.7	116	Ig heavy chain V reg 1.64e-65
18	542	56.7	122	Ig heavy chain V reg 5.64e-65
19	538	56.3	119	Ig heavy chain V reg 2.42e-64
20	538	56.3	123	Ig heavy chain V-1 reg 2.42e-64

21	537	56.2	98	Ig heavy chain V reg 3.49e-64
22	537	56.2	116	Ig heavy chain V reg 3.49e-64
23	537	56.2	123	Ig heavy chain V-1 reg 7.23e-64
24	535	56.0	98	Ig heavy chain V-1 reg 7.23e-64
25	535	56.0	119	Ig heavy chain V reg 7.23e-64
26	531	55.5	113	Ig heavy chain V reg 7.23e-64
27	527	55.1	125	Ig heavy chain V reg 1.32e-63
28	518	54.3	125	Ig heavy chain V reg 1.32e-63
29	515	53.9	98	Ig heavy chain V reg 1.32e-63
30	515	53.9	129	Ig heavy chain V reg 1.32e-63
31	513	53.7	122	Ig heavy chain V reg 1.32e-63
32	510	53.3	131	Ig heavy chain V reg 6.41e-60
33	505	52.8	97	Ig heavy chain V reg 3.93e-59
34	503	52.6	124	Ig heavy chain V reg 8.11e-59
35	499	52.2	122	Ig heavy chain V reg 3.46e-58
36	494	51.7	148	Ig heavy chain V reg 2.11e-57
37	490	51.3	108	Ig heavy chain V reg 8.98e-57
38	489	51.2	117	Ig heavy chain V-1 reg 1.29e-56
39	487	50.9	142	Ig heavy chain V reg 2.45e-56
40	484	50.6	136	Ig heavy chain V-1 reg 2.45e-56
41	483	50.5	116	Ig heavy chain V reg 1.13e-55
42	481	50.3	98	Ig heavy chain V-1 reg 2.32e-55
43	475	49.7	109	Ig heavy chain V reg 2.02e-54
44	475	49.7	119	Ig heavy chain V reg 2.02e-54
45	474	49.6	126	Ig heavy chain V reg 2.90e-54

ALIGNMENTS

RESULT 1
ENTRY PH0957
TITLE Ig heavy chain V region (G6+ CLL-BRA) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-1996
ACCESSIONS PH0957
REFERENCE PH0952
#authors Martin, T.; Duffy, S.F.; Carson, D.A.; Kipps, T.J.
#journal J Exp Med (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MIM:2202880
#accession PH0957
#status nucleic acid sequence not shown
#molecule_type DNA
#residues 1-125 #label MAP
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30 #region framework 1\
31-35 #domain immunoglobulin homology #label IMV\
36-50 #region complementarity-determining 1\
51-67 #region complementarity-determining 2\
68-98 #region framework 2\
99-113 #region complementarity-determining 3
SUMMARY #length 125 #checksum 8143
Query Match 56.1%; Score 632; DB 7; Length 125;
Best Local Similarity 72.9%; Pred. No. 2.62e-79;
Matches 37; Conservative 15; Mismatches 12; Indels 9; Gaps 4;

Db	1	gqlrvgsgavkpggsvkscasgttssyainvrragpggglewmgdlpigtan	59
Cy	1	EVQLLESGAEVPRKPGSSVKASQCTFGHVTWVQAPQCGLEWMEGSLPFGSAN	60
Db	60	rag----kfgrvttadestntarmolsslrsoatvrrycardg---csqsgscfxfw	112
Cy	61	YAOYNAKRFDPVSIAPSTSTSFIELSNLPSNQTAVYVCAAPPVPCASGATYP-GFF	119
Db	113	dwggglvtvss	125
Cy	126	QEWGGTLTVSS	126


```

RESULT 5
ENTRY
TITLE Ig heavy chain V-1 region (AND) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996
ACCESSIONS B33548
REFERENCE
#authors Kippes, T.J., Tomhave, E., Pratt, L.F., Daffy, S., Chen, F.P., Carson, D.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin heavy chain
variable region gene expressed at high frequency in chronic
lymphocytic leukemia.
#cross-references MUID:89345575
#accession B33548
#status preliminary; nucleic acid sequence not shown; not
compared with conceptual translation
##molecule_type DNA
##residues 1-126 #label KIP
##experimental_source the sequence was determined from the
differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
Query Match 50.4%, Score 575, DB 7, Length 126,
Best Local Similarity 57.4%, Pred. No. 3 27e-70,
Matches 89; Conservative 18; Mismatches 19; Indels 6; Gaps 3;
Db 1 gqqlv-gsgaevkpgssvskasggtfssyaiswvrgapggglewmg-wisvy-nod 75
QY 1 EVQLLESGAEEVRRPQSSVKASGGIFSGHVIWVRQAPGGGLEWNGESIPFGSAN 60
Db 60 yag----kfgqvttadststststststststststststststststststst 114
QY 61 YAGNYAKKFPKPVSVIACESTISFIELSNLPSCDTAVVYCAPPPPYCSAGPCYPGPFQ 120
Db 115 vwqlgtttvss 126
QY 121 QWGGTLTVSS 132
RESULT 6
ENTRY
TITLE anti-FP2 erythrocyte autoantibody heavy chain precursor
human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change
26-Apr-1996
ACCESSIONS PL0105
REFERENCE
#authors Silberstein, L.E.; Litwin, S.; Carmack, C.E.
#journal J. Exp. Med. (1989) 169:1631-1643
#title Peliosis of variable region genes expressed by a human B
cell lymphoma secreting pathologic anti-pr-2 erythrocyte
autoantibodies.
#cross-references MUID:89235583
#accession PL0105
##molecule_type mRNA
##residues 1-160 #label SIL
##note the authors translated the codon GAC for residues 108
and 109 as Glu
COMMENT The antibody is one of the cold agglutinins that preferentially
bind red blood cell membrane antigens at low temperature, causing
cold agglutinin disease (CAD).
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS autoantibody; hemagglutinin
FEATURE

```

```

1-19 #domain signal sequence #status predicted #label SIG
34-117 #domain immunoglobulin homology #label IMM
49-54 #region complementarity-determining 1\
69-84 #region complementarity-determining 2\
118-131 #domain D region #label DRG
132-144 #domain J4 segment #label JSC
145-160 #domain C region #label CRG
SUMMARY #length 160 #checksum 3900
Query Match 59.4%, Score 567, DB 7, Length 160;
Best Local Similarity 64.4%, Pred. No. 6 10e-69,
Matches 85; Conservative 24; Mismatches 16; Indels 7; Gaps 7;
Db 20 gqqlv-gsgaevkpgssvskasggtfssyaiswvrgapggglewmg-wisvy-nod 75
QY 1 EVQLLESGAEEVRRPQSSVKASGGIFSGHVIWVRQAPGGGLEWNGESIPFGSAN 60
Db 77 -t-nyagqlgrvtmttdststststststststststststststststststst 132
QY 61 YAGNYAKKFPKPVSVIACESTISFIELSNLPSCDTAVVYCAPPPPYCSAGPCYPGPFQ 120
Db 133 ywgggtltvss 144
QY 121 QWGGTLTVSS 132
RESULT 7
ENTRY
TITLE Ig heavy chain V region (G6+ T-142) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
ACCESSIONS PH0962
REFERENCE
#authors Martin, J., Daffy, S.F., Carson, F.A., Kippes, T.J.
#journal G. Exp. Med. (1992) 175:983-991
#title Evidence for somatic selection of natural autoantibodies.
#cross-references MUID:9202880
#accession PH0962
#status nucleic acid sequence not shown
##molecule_type DNA
##residues 1-120 #label MAR
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
1-30 #region framework 1\
15-98 #domain immunoglobulin homology #label IMM
31-35 #region complementarity-determining 1\
36-50 #region framework 2\
51-67 #region complementarity-determining 2\
68-98 #region framework 3\
99-108 #region complementarity-determining 3
SUMMARY #length 120 #checksum 5559
Query Match 59.4%, Score 566, DB 7, Length 120;
Best Local Similarity 72.0%, Pred. No. 8.80e-69;
Matches 95; Conservative 14; Mismatches 11; Indels 12; Gaps 5;
Db 1 gqqlv-gsgaevkpgssvskasggtfssyaiswvrgapggglewmg-wisvy-nod 59
QY 1 EVQLLESGAEEVRRPQSSVKASGGIFSGHVIWVRQAPGGGLEWNGESIPFGSAN 60
Db 60 yag--kfgqvttadststststststststststststststststststst 109
QY 61 YAGNYAKKFPKPVSVIACESTISFIELSNLPSCDTAVVYCAPPPPYCSAGPCYPGPFQ 120
Db 109 ywgggtltvss 120
QY 121 QWGGTLTVSS 132
RESULT 8
ENTRY
TITLE

```

Thu Feb 26 07:03:36 1998

```

TITLE
ORGANISM
DATE
Iq heavy chain V region (G6+ CLL-SIC) - human (fragment)
#formal_name Homo sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
PH0953
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:92202880
#accession
PH0953
#status
#molecule_type DNA
#residues
1-135 #label MAR
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS
heterotetramer; immunoglobulin
FEATURE
1-30
15-98
31-35
36-50
51-67
68-98
99-123
#length 135 #checksum 2318
SUMMARY
Query Match 58.6%; Score 560; DB 7; Length 135;
Best Local Similarity 72.4%; Pred. No. 7.90e-68;
Matches 84; Conservative 16; Mismatches 8; Indels 8; Gaps 4;
Db 1 qvqlv-qsgaevkpgssvskvscasgtfssyaiswvrqpggglevmgqilpigtan 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1 EVQLLEQSGAEVRKPGSSVKVSKASGTFSGHVTWVRQAPGQGLEWMGESIPIFGSAN 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 yaq---kfggrvtideststymelsslrstedtavyycarg--ycg-gdcys 108
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 YAQNYAQKFRDVRSLIADESTSTFIELNLSRSDDTAVYYCARDPPRYCSAGRCYP 116
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
RESULT 9
ENTRY
TITLE
ORGANISM
DATE
PH0954
Iq heavy chain V region (G6+ CLL-HEN) - human (fragment)
#formal_name Homo sapiens #common_name man
17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change
16-Aug-1996
PH0954
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:92202880
#accession
PH0954
#status
#molecule_type DNA
#residues
1-132 #label MAR
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS
heterotetramer; immunoglobulin
FEATURE
1-30
15-98
31-35
36-50
51-67
68-98
99-120
#length 132 #checksum 9232
SUMMARY
Query Match 58.5%; Score 559; DB 7; Length 132;
Best Local Similarity 66.4%; Pred. No. 1.14e-67;
Matches 91; Conservative 18; Mismatches 18; Indels 10; Gaps 5;
Db 1 qvqlv-qsgaevkpgssvskvscasgtfssyaiswvrqpggglevmgqilpigtan 59
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

```

```

Qy 1 EVQLLEQSGAEVRKPGSSVKVSKASGTFSGHVTWVRQAPGQGLEWMGESIPIFGSAN 60
Db 60 yaq---kfggrvtideststymelsslrstedtavyycarphasidlfwsqyyfny 115
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 YAQNYAQKFRDVRSLIADESTSTFIELNLSRSDDTAVYYCARDPPRYCSAGRCYP 119
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 116 YVGMdvwgqgtttvss 132
:||||:||||:
Qy 120 ---QQ-WGQGTILVTVSS 132
:||||:||||:
RESULT 10
ENTRY
TITLE
ORGANISM
DATE
S36260
Iq heavy chain V region (clone alpha-CEA4-8A) - human
(fragment)
#formal_name Homo sapiens #common_name man
03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996
ACCESSIONS
REFERENCE
#authors
Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Rye, J.M.;
Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
G.
#journal
EMBO J. (1993) 12:725-734
#title
Human anti-self antibodies with high specificity from phage
display libraries.
#accession
S36260
#status
preliminary; nucleic acid sequence not shown
#molecule_type mRNA
#residues
1-129 #label GRI
#cross-references EMBL:Z18851
CLASSIFICATION
#superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS
heterotetramer; immunoglobulin
FEATURE
15-98
#domain immunoglobulin homology #label IMM
SUMMARY
#length 129 #checksum 9521
Query Match 57.6%; Score 551; DB 7; Length 129;
Best Local Similarity 61.9%; Pred. No. 2.11e-66;
Matches 83; Conservative 26; Mismatches 18; Indels 7; Gaps 7;
Db 1 qvqlv-qsgaevkpgssvskvscasgtfssyaiswvrqpggglewmq-wisay-dnn 57
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1 EVQLLEQSGAEVRKPGSSVKVSKASGTFSGHVTWVRQAPGQGLEWMGESIPIFGSAN 60
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 58 -t-nyacklqgrvtmttdststymelsslrddlavyyccardsfqycsstscqyyvy 115
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 61 YAQNYAQKFRDVRSLIADESTSTFIELNLSRSDDTAVYYCARDPPRYCSAGRCYP 119
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 116 mdvwgkattvss 129
:||||:||||:
Qy 120 QQ-WGQGTILVTVSS 132
:||||:||||:
RESULT 11
ENTRY
TITLE
ORGANISM
DATE
S36261
Iq heavy chain V region (clone alpha-TNF-E7) - human
(fragment)
#formal_name Homo sapiens #common_name man
03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change
16-Aug-1996
ACCESSIONS
REFERENCE
#authors
Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Rye, J.M.;
Embleton, M.J.; McCafferty, J.; Baier, M.; Holliger, K.P.;
Gorick, B.D.; Hughes-Jones, N.C.; Hoogenboom, H.R.; Winter,
G.
#journal
EMBO J. (1993) 12:725-734
#title
Human anti-self antibodies with high specificity from phage
display libraries.
#accession
S36261
#status
preliminary; nucleic acid sequence not shown

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```

#molecule_type mRNA
#residues 1-116 ##label GRI
##cross-references EMBL:Z18841
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 116 #checksum 7971

Query Match 57.4%; Score 549; DB 7; Length 116;
Best Local Similarity 74.3%; Pred. No. 4.39e-66;
Matches 81; Conservative 14; Mismatches 8; Indels 6; Gaps 3;

Db 1 qvqlv-qsgaevkpgssvksckasggtfssyaisvswrqpqgglewmggilpifatan 59
QY 1 EVQLLEQSGAEVRFKPGSSVKSSCKASGTFSGHVTITWVQAPQGGLWMGSGIPFISAN 60

Db 60 yaq----kfggrvtitadeststamelslrsdtaavycargplrgy 104
QY 61 YACNVAKKFPDVRYSIIADESTSTSFIELSNLPSDTAVVYCAPTPP-Y 108

RESULT 12
ENTRY A49590 #type fragment
TITLE Ig heavy chain V region (ACHSV1, clone 15) - human (fragment)
ORGANISM #formal_name Homo sapiens #common_name man
DATE 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change
23-May-1997

ACCESSIONS A49590
REFERENCE
#authors Burton, R.; Williamson, P. A.; Sanna, P. P.; Bloom, P. E.;
Burton, D.R.
#journal Proc Natl. Acad. Sci. U.S.A. (1994) 91:355-359
#title Recombinant human Fab to glycoprotein D neutralizes
infectivity and prevents cell-to-cell transmission of
herpes simplex viruses 1 and 2 in vitro.
#cross-references MUID:94105168
#accession A49590
#status preliminary; not compared with conceptual translation
#residues 1-121 ##label BUP
#cross-references NCBI:P141850
#experimental_source bone marrow lymphocytes
#note sequence extracted from NCBI backbone
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
11-94
SUMMARY
#domain immunoglobulin homology #label IMM
#length 121 #checksum 6226

Query Match 57.1%; Score 546; DB 7; Length 121;
Best Local Similarity 64.3%; Pred. No. 1.31e-65;
Matches 81; Conservative 20; Mismatches 19; Indels 6; Gaps 4;

Db 2 esgaevkpgssvksckasggtfssyaisvswrqpqgglewmggilpifatan-b-a 57
QY 7 QSGAEVRFKPGSSVKSSCKASGTFSGHVTITWVQAPQGGLWMGSGIPFISAN 66

Db 58 qkfggrvtitadeststamelslrsdtaavycar-vg-yctngsglsgmdvwgggt 115
QY 57 QKFPQVSIADSTSTSFIELSNLPSDTAVVYCAPTPP-Y 126

Db 116 tvivss 121
QY 127 LVTVSS 132

RESULT 13
ENTRY S46394 #type complete
TITLE Ig heavy chain V region - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change
23-May-1997

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ACCESSIONS S46394
REFERENCE
#authors Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
#journal J. Mol. Biol. (1994) 239:68-78
#title In vitro assembly of repertoires of antibody chains on the
surface of phage by renaturation.
#accession S46394
#status preliminary
#molecule_type DNA
#residues 1-132 ##label FIG
#cross-references EMBL:Z31681
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 132 #molecular_weight 14293 #checksum 7515

Query Match 57.1%; Score 546; DB 7; Length 132;
Best Local Similarity 65.0%; Pred. No. 1.31e-65;
Matches 89; Conservative 20; Mismatches 18; Indels 10; Gaps 7;

Db 1 qvqlv-qsgaevkpgssvksckasggtfssyaisvswrqpqgglewmggilpifatan 59
QY 1 EVQLLEQSGAEVRFKPGSSVKSSCKASGTFSGHVTITWVQAPQGGLWMGSGIPFISAN 60

Db 60 yaq----kfggrvtitadeststamelslrsdtaavycar-vg-yctngsglsgmdvwgggt 115
QY 61 YACNVAKKFPDVRYSIIADESTSTSFIELSNLPSDTAVVYCAPTPP-Y 118

Db 116 tvivss 121
QY 119 F--QQ-WGQGLTVTVSS 132

RESULT 14
ENTRY C33548 #type complete
TITLE Ig heavy chain V-1 region (783) - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE 17-Jan-1990 #sequence_revision 17-Jan-1990 #text_change
16-Aug-1996

ACCESSIONS C33548
REFERENCE
#authors Kipps, T. J.; Tomhave, E.; Pratt, L.F.; Duffy, S.; Chen, P.P.;
Carson, D.A.
#journal Proc. Natl. Acad. Sci. U.S.A. (1989) 86:5913-5917
#title Developmentally restricted immunoglobulin heavy chain
variable region gene expressed at high frequency in chronic
lymphocytic leukemia.
#cross-references MUID:89345575
#accession C33548
#status preliminary; nucleic acid sequence not shown; not
compared with conceptual translation
#molecule_type DNA
#residues 1-133 ##label KIP
#experimental_source differentiated gene
CLASSIFICATION #superfamily immunoglobulin V region; immunoglobulin homology
KEYWORDS heterotetramer; immunoglobulin
FEATURE
15-98
SUMMARY
#domain immunoglobulin homology #label IMM
#length 133 #molecular_weight 14220 #checksum 1389

Query Match 57.0%; Score 545; DB 7; Length 133;
Best Local Similarity 66.4%; Pred. No. 1.89e-65;
Matches 93; Conservative 20; Mismatches 12; Indels 15; Gaps 9;

Db 1 qvqlv-qsgaevkpgssvksckasggtfssyaisvswrqpqgglewmggilpifatan 59
QY 1 EVQLLEQSGAEVRFKPGSSVKSSCKASGTFSGHVTITWVQAPQGGLWMGSGIPFISAN 60

Db 60 yaq----kfggrvtitadeststamelslrsdtaavycar-vg-yctngsglsgmdvwgggt 113
QY 61 YACNVAKKFPDVRYSIIADESTSTSFIELSNLPSDTAVVYCAPTPP-Y 117

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Db      114 dyyygmdvwaqggtvtvs 133
::      : ||||| |||||
Qy      118 ---PF-QQ-WGQGLTVVSS 132
::      : ||||| |||||

RESULT      15
ENTRY      S14683      #type complete
TITLE      Ig mu chain precursor, membrane-bound (clone 201) - human
ORGANISM   Homo sapiens #common_name man
DATE       31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change
          16-Aug-1996
ACCESSIONS S14683; S08047
REFERENCE   S14683
AUTHORS     Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
JOURNAL     Nucleic Acids Res. (1990) 18:4278
TITLE       Complete nucleotide sequence of the membrane form of the
            human IgM heavy chain.
CROSS-REFERENCES MUID:90332450
ACCESSION    S14683
MOLECULE_TYPE mRNA
RESIDUES     1-627 #label FRI
CROSS-REFERENCES EMBL:X17115
CLASSIFICATION #superfamily immunoglobulin C region; immunoglobulin homology
KEYWORDS      immunoglobulin; membrane protein
FEATURE       1-15      #domain signal sequence #status predicted #label SIG\
16-627         #product Ig mu chain #status predicted #label MAT\
34-117         #domain immunoglobulin homology #label IMM
              #length 627 #molecular_weight 68510 #checksum 8581

SUMMARY
Query Match      57.0%; Score 545; DB 7; Length 627;
Best Local Similarity 66.4%; Pred. NO. 1,896-65;
Matches          93; Conservative 20; Mismatches 12; Indels 15; Gaps 9;

Db      20 qvqlv-qsaevkpgssvkscasqgtffsyaaiswvrqpgqglewmqgiipqtan 78
::      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      1 EVOLLEQSGAEVRKPGSSVKVSKASGGTFSGHVITVYRQAPGQGLEWMGESIPFGSAN 60
::      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db      79 yag---kfgrrytltadestaymelsslrtsedtavvycaaktgiiqpy-ssgw-yyps 132
::      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy      61 YAQYNAQKFRDRVYIIADESTSTSFIELSNLRSDDTAVVYICARDP--PRYCSAGRCYP-G 117
::      : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db      133 dyyygmdvwaqggtvtvs 152
::      : ||||| |||||
Qy      118 ---PF-QQ-WGQGLTVVSS 132
::      : ||||| |||||

```

Search completed: Tue Feb 24 07:02:57 1998
Job time : 32 secs.

WILEY
***** (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Tue Feb 24 07:01:43 1998; MasPar time 5.55 Seconds
Tabular output not generated. 504.423 Million cell updates/sec

Title: >US-08-844-215-1
Description: (1-132) from US08844215.pep
Perfect Score: 956
Sequence: 1 EVQLLEQSGAEVKKPKQSSVK... PCYPGFFQWQGILVTYSS 132

Scoring table: PAM 150
Gap 11
Searched: 59021 seqs, 21210388 residues
Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot34
1:part1 2:part2 3:part3 4:part4 5:part5 6:part6 7:part7
8:part8 9:part9 10:part10 11:part11
Statistics: Mean 42 359; Variance 75 508; scale 0.561

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES							
Result No.	Score	Query		DB	ID	Description	Pred No.
		Match	Length				
1	489	51	2	5	HV1A_HUMAN	IG HEAVY CHAIN V-I PE	1 226-81
2	445	46.5		117	HV1B_HUMAN	IG HEAVY CHAIN PRECUR	7 546-72
3	440	46.0		117	HV1G_HUMAN	IG HEAVY CHAIN PRECUR	9 656-71
4	427	44.7		114	HV1G_MOUSE	IG HEAVY CHAIN V REGI	7 100-68
5	424	44.4		143	HV1C_HUMAN	IG HEAVY CHAIN PRECUR	3 306-67
6	416	43.5		140	HV02_MOUSE	IG HEAVY CHAIN PRECUR	1 906-65
7	412	43.1		120	HV03_MOUSE	IG HEAVY CHAIN V REGI	1 446-64
8	406	42.5		124	HV1E_HUMAN	IG HEAVY CHAIN V-I PE	3 006-63
9	405	42.4		125	HV1F_HUMAN	IG HEAVY CHAIN V-I PE	4 976-63
10	405	42.4		126	HV3K_HUMAN	IG HEAVY CHAIN V-III	4 976-63
11	394	41.2		121	HV01_MOUSE	IG HEAVY CHAIN V REGI	1 276-60
12	394	41.2		122	HV3G_HUMAN	IG HEAVY CHAIN V-III	1 276-60
13	384	40.2		117	HV05_MOUSE	IG HEAVY CHAIN PRECUR	1 946-58
14	383	40.1		124	HV1D_HUMAN	IG HEAVY CHAIN V-I PE	3 216-58
15	378	39.5		117	HV13_MOUSE	IG HEAVY CHAIN V REGI	3 946-57
16	377	39.4		117	HV04_MOUSE	IG HEAVY CHAIN PRECUR	6 506-57
17	377	39.4		117	HV12_MOUSE	IG HEAVY CHAIN V REGI	6 506-57
18	372	38.9		117	HV52_MOUSE	IG HEAVY CHAIN PRECUR	7 946-56
19	368	38.5		117	HV14_MOUSE	IG HEAVY CHAIN PRECUR	5 866-55
20	368	38.5		118	HV51_MOUSE	IG HEAVY CHAIN PRECUR	5 866-55
21	367	38.4		117	HV06_MOUSE	IG HEAVY CHAIN V REGI	9 666-55
22	365	38.2		139	HV07_MOUSE	IG HEAVY CHAIN PRECUR	2 626-54

22	364	38.1	120	5	HV50_MOUSE	IG HEAVY CHAIN V REGI	4.32e-54
24	364	38.1	138	5	HV48_MOUSE	IG HEAVY CHAIN PRECUR	4.32e-54
25	361	37.8	142	5	HV01_PAT	IG HEAVY CHAIN PRECUR	1.93e-53
26	359	37.4	137	5	HV11_MOUSE	IG HEAVY CHAIN PRECUR	8.58e-53
27	357	37.3	122	5	HV38_HUMAN	IG HEAVY CHAIN V-III	1.41e-52
28	356	37.2	119	5	HV38_HUMAN	IG HEAVY CHAIN V-III	2.22e-52
29	356	37.2	120	5	HV18_HUMAN	IG HEAVY CHAIN V-I PE	2.32e-52
30	352	36.8	117	5	HV45_MOUSE	IG HEAVY CHAIN PRECUR	1.70e-51
31	350	36.6	117	5	HV09_MOUSE	IG HEAVY CHAIN PRECUR	4.58e-51
32	346	36.2	119	5	HV31_HUMAN	IG HEAVY CHAIN V-III	3.33e-50
33	345	36.1	119	5	HV31_HUMAN	IG HEAVY CHAIN V-III	5.46e-50
34	344	36.0	113	5	HV30_MOUSE	IG HEAVY CHAIN V-III	8.96e-50
35	344	36.0	115	5	HV26_MOUSE	IG HEAVY CHAIN PRECUR	8.96e-50
36	344	36.0	144	5	HV28_MOUSE	IG HEAVY CHAIN V-III	3.96e-49
37	341	35.7	113	5	HV28_MOUSE	IG HEAVY CHAIN V-III	3.96e-49
38	341	35.7	113	5	HV03_CAPAU	IG HEAVY CHAIN PRECUR	6.49e-49
39	340	35.6	117	5	HV03_CAPAU	IG HEAVY CHAIN PRECUR	6.49e-49
40	340	35.6	117	5	HV3C_HUMAN	IG HEAVY CHAIN PRECUR	6.49e-49
41	340	35.6	117	5	HV10_MOUSE	IG HEAVY CHAIN PRECUR	6.49e-49
42	340	35.6	120	5	HV3E_HUMAN	IG HEAVY CHAIN V-III	6.49e-49
43	340	35.6	121	5	HV3J_HUMAN	IG HEAVY CHAIN V-III	6.49e-49
44	337	35.3	113	5	HV34_MOUSE	IG HEAVY CHAIN V REGI	2.86e-48
45	334	34.9	115	5	HV33_MOUSE	IG HEAVY CHAIN V-III	1.26e-47

ALIGNMENTS

RESULT 1
ID HV1A_HUMAN STANDARD: PRT; 117 AA.
AC P01742;
DT 21-JUL-1986 (REL. 01, CREATED)
DI 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DE 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
DE IG HEAVY CHAIN V-I REGION (EU).
OS HOMO SAPIENS (HUMAN).
CC EUPARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC EUTHERIA; PRIMATES.
PN [1]
RP SEQUENCE.
RX MEDLINE: 71064024.
RA CUNNINGHAM R A, PITTSHAMSEP M, GALL W E, GOTTILIEB P D..
RA WAXDAL M J., EDELMAN G M..
PL BIOCHEMISTRY 9:3161-3170(1970).
RN [2]
RP DISULFIDE BOND.
RX MEDLINE: 71064027.
RA GALL W E., EDELMAN G M..
PL BIOCHEMISTRY 9:3188-3196(1970).
CC -!- THE SEQUENCE OF THE GAMMA-1 C REGION OF THIS MYELOMA PROTEIN HAS
CC ALSO BEEN DETERMINED.
DR PIR; A02023; GIHEU.
DF HSSP; P01810; 1FVB.
KW IMMUNOGLOBULIN V REGION.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT NONTER 117 117
SQ SEQUENCE 117 AA: 12477 MW: 108367.75 PCQD2:
Query Match 51.2%, Score 489, DB 5; Length 117;
Best Local Similarity 70.6%, Pred. No. 1,226-81;
Matches 72; Conservative 16; Mismatches 9, Indels 5, Gaps 2.
CU 1 qvqlly-qsgaevkkgssvskvskasgttfsadilwvrdagqgylwmgdlypmlfppa 59
...
QY 1 EVQLLEQSGAEVKKPKQSSVKVSKASGTTISGRVITWVPAPQGLLEWMSIESPIFGSAN 60
...
Db 60 yaq----kfqrvtidestntaymelslrdsdtafyca 97
...
QY 61 YAQYAAQKPEFFRVSTIADESTISFIELSNLPDSTAYVYCA 102
...
RESULT 2
ID HV1B_HUMAN STANDARD: PRT; 117 AA.

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RESULT      4
AC ID       HV00_MOUSE          STANDARD;             PRT:   114 AA.
AC PO1741;
DE DT       21-JUL-1986 (PEL 01, CREATED)
DE DT       21-JUL-1986 (PEL 01, LAST SEQUENCE UPDATE)
DE DT       21-JUL-1986 (PEL 01, LAST ANNOTATION UPDATE)
DE DT       IG HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
OS MUS MUSCULUS (MOUSE)
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE.
PC STRAIN-A/J;
RX MEDLINE; 79195438.
CPA CAPPA J B . NISCHOFF A.;
PXA EVOLVED GENE EXPRESSION IN THE HEAVY CHAIN V REGION OF THE IGG1
DDE IT - ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF THE IGG1
DE DE SUBSEQUENCE. THERE WAS NO HELIPSEGENEITY IN THE HEAVY CHAIN V REGION
OS CC SEQUENCE.
OC CC
PIR: AQ2022; GIMSAA..
HSP: PQ1772; IFGV..
IMMUNOGLOBULIN V REGION; ANTIARSONATE ANTIBODY.
NON_TER    114     114
SEQUENCE   114 AA; 12555 MW; 1AQ27FD CRC32;

Query Match           44.7% Score 427; DB 5; Length 114;
Best Local Similarity 63.3%; Pred.No. 7,19e-68;
Matches 69; Conservative 22; Mismatches 12; Indels 6; Gaps
                                60
dDb 1 evql-qdsgealvkaqssvkmsckatdyfssyelywvrqpapqalelaryis--sssa 56
    ||||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :||
QY 1 EVQLLEGSGAEVRFGSSVSKVSCASGCTFSGHVITWVCAPGCGLEWKGESIFTPESAN 60

dDb 57 yp-dyagkfgrvtadestlnlaymelslsrscdtayvcavvisy 104
    ||||| :||||| :||| :||||| :||||| :||||| :||||| :||||| :||
QY 61 YAGYAGKEFQRVSIIADESTISTSFIELNLSGLTAVYYCA-PGPTRY 104


RESULT      5
AC ID       HVIC_HUMAN          STANDARD;             PRT:   143 AA.
AC PO1744;
DE DT       21-JUL-1986 (PEL 01, CREATED)
DE DT       21-JUL-1986 (PEL 01, LAST SEQUENCE UPDATE)
DE DT       01-NOV-1980 (PEL 16, LAST ANNOTATION UPDATE)
DE DE IG HEAVY CHAIN PRECURSOR V-I REGION (ND) (FRAGMENTS).
OS HUMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
PC MEDLINE; 83065234.
CPA KENTEN J.H., MULLGAARD H.V., ROBERTSON M.L., DENVERSHIRE R.P., VINCE J.J.
PXA BELL L.O., GOULD H.J.;
PRL PROC. NATL ACAD. SCI U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 16-142.
DE BENNICHT H.H., JOHANSSON S.G.O., VON BAHR-LINDSTROM H.;
DE (IN) IMMEDIATE HYPERSENSITIVITY: MODERN CONCEPTS AND DEVELOPMENTS.
DE RACH M.K., ED., PP 146, MACGER DEKKER, NEW YORK, (1978).
OS - THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DE P1- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
OS P1- THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DE HSP: PQ1607; IFGV..
IMMUNOGLOBULIN V REGION; SIGNAL.
NON_CONS   4       5
FT SIGNAL         1 15
FT CHAIN          16 143
FT M-D_RES        16 16
FT DISULFID       37 111
FT CONFLICT       17 17
FT CONFLICT       49 50
FT CONFLICT       62 64
FT CONFLICT       121 121
FT NON_TER       143 143
IG HEAVY CHAIN V REGION (ND);
PYRROLIDONE CARBOXYLIC AMIDE.
T-S-V (IN REF. 2);
TH-S-HI (IN REF. 2);
VG-S-GV (IN REF. 2);
MISSING (IN REF. 2);

```

SQ SEQUENCE 143 AA: 16051 MW: 60605EL3 CPC32;
 Query Match 44.4%, Score 424, DR 5, Length 143;
 Best Local Similarity 52.6%, Pred. No. 3, 30e-67;
 Matches 70, Conservative 24, Mismatches 23, Indels 6, Gaps 6;
 Db 15 qqlv-gsgaevkpgssvskvskasggtfsgyibwlrqgphalewq-winp-nsgg 72
 QY 1 EVOLLEQSGAEVPRKPGSSVKVSKASGTFSGHVTWVPAQPGQGLEWMGESIPFGSAN 60
 Db 73 t-nvaprfggvmtmdasfstaymdlrslrdsdsvfycakspfdsvyndysyl 130
 QY 61 YACNYAKKPEPVPVSIADSTSTFIELSNLPSDTAVVYCAPPPYCSA-SPVYPPGF 119
 Db 131 dwgggtttvtss 143
 QY 120 QWGGGTLTVSS 132
 RESULT 6
 ID HV02-MOUSE STANDARD: PPT: 140 AA
 AC P01746;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN PRECURSOR V REGION (93G7).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A/J;
 PX MEDLINE: P0152919;
 RA SIMS J., PARRITTS T.H., ESTESS P., SLAUGHTER C., TUCKER P.W.,
 RA CAPRA J.D., 309-311(1982).
 RL SCIENCE 216:309-311(1982).
 DR EMRL: J00493; G195007;
 DP PIP: A02028; HVMG67
 DP HSSP: P01789; 6FAB
 KW IMMUNOGLOBULIN V REGION: ANTIAPSONATE ANTIBODY; HYPERIDOMA; SIGNAL.
 FT SIGNAL 1 19 IG HEAVY CHAIN V REGION (93G7).
 FT CHAIN 20 140
 FT NON-TER 140 140
 SQ SEQUENCE 140 AA: 15514 MW: 0700DSC8 CPC32;
 Query Match 43.5%, Score 416, DR 5, Length 140;
 Best Local Similarity 51.5%, Pred. No. 1, 9e-65;
 Matches 68, Conservative 30, Mismatches 23, Indels 11, Gaps 10;
 Db 20 evql-qsgaelvragssvskmskasytftsyginwvkprgqglewlg-yinp-gng- 75
 QY 1 EVOLLEQSGAEVPRKPGSSVKVSKASGTFSGHVTWVPAQPGQGLEWMGESIPFGSAN 60
 Db 76 yinp-nckkfgkttldvksstaysmqlrsltsdsaryfcar--shyvg-gs-y-df-d 129
 QY 61 YACNYAKKPEPVPVSIADSTSTFIELSNLPSDTAVVYCAPPPYCSA-SPVYPPGF 129
 Db 129 ywgggtttvtss 140
 QY 121 QWGGGTLTVSS 132
 RESULT 7
 ID HV03-MOUSE STANDARD: PPT: 120 AA
 AC P01747;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V REGION (36-65).
 OS MUS MUSCULUS (MOUSE).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; RODENTIA.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE: 83131846;
 RA STEKEVITZ M., GEFTER M.L., PROFFER P., PIBLET R.,
 RA MAPSHAKI-ROTHSTEIN A.,
 PL EUP 3 IMMUNOL 12:1023-1022(1992).
 CC -1- FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER DIFFERENTIATED GENES
 CC THAT HYPERIDOME TO THIS ONE, THE AUTHORS CONCLUDE THAT ALL OF
 CC THESE V REGIONS HAVE REAPPRANGED TO THE SAME J SEGMENT, JH2.
 DR PIR: A02028; HVMG67.
 DR HSSP: P01789; 6FAB.
 KW IMMUNOGLOBULIN V REGION: ANTIAPSONATE ANTIBODY; HYPERIDOMA.
 FT NON-TER 120 120
 SQ SEQUENCE 120 AA: 13397 MW: BRAR0CA1 CPC32;
 Query Match 43.1%, Score 412, DR 5, Length 120;
 Best Local Similarity 50.4%, Pred. No. 1, 44e-64;
 Matches 66, Conservative 32, Mismatches 22, Indels 11, Gaps 10;
 Db 1 vql-qsgaelvragssvskmskasytftsyginwvkprgqglewlg-yinp-gng-y 56
 QY 2 VOLLEQSGAEVPRKPGSSVKVSKASGTFSGHVTWVPAQPGQGLEWMGESIPFGSAN 61
 Db 57 t-ynckkfgkttldvksstaysmqlrsltsdsaryfcar-sv-yyg-gs-y-yfay 109
 QY 62 AANYAKKPEPVPVSIADSTSTFIELSNLPSDTAVVYCAPPPYCSA-SPVYPPGF 121
 Db 110 wgggtttvtss 120
 QY 122 QWGGGTLTVSS 132
 RESULT 8
 ID HV16-HUMAN STANDARD: PPT: 124 AA.
 AC P01761;
 DT 21-JUL-1986 (REL. 01, CREATED)
 DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
 DT 21-JUL-1986 (REL. 01, LAST ANNOTATION UPDATE)
 DE IG HEAVY CHAIN V-I REGION (SIE)
 OS HOMO SAPIENS (HUMAN).
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
 OC EUTHERIA; PRIMATES.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE: 82046599.
 RA ANDREWS D.W., CAPRA J.D.,
 RA BIOCHEMISTRY 20:5822-5830(1981).
 CC -1- THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN
 CC ACTIVITY.
 DR PIR: A02044; MHUS1.
 DR HSSP: P01857; 2FGW.
 KW IMMUNOGLOBULIN V REGION.
 FT NON-TER 124 124
 SQ SEQUENCE 124 AA: 13732 MW: CLE2663D CPC32;
 Query Match 42.9%, Score 406, DR 5, Length 124;
 Best Local Similarity 50.8%, Pred. No. 4, 00e-63;
 Matches 67, Conservative 27, Mismatches 28, Indels 10, Gaps 8;
 Db 1 qqlv-gsgaevkpgssvskvskasggtfsgyibwlrqgphalewq-winp-nsgg 57
 QY 1 EVOLLEQSGAEVPRKPGSSVKVSKASGTFSGHVTWVPAQPGQGLEWMGESIPFGSAN 60
 Db 58 fggwyik-worvvelskpsfndaymelvalfnedavvycarow-k-ggavvmp--fd 110
 QY 61 YACNYAKKPEPVPVSIADSTSTFIELSNLPSDTAVVYCAPPPYCSA-SPVYPPGF 120
 Db 111 ywgggtttvtss 122
 QY 121 QWGGGTLTVSS 132
 RESULT 9

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FT HELIX      29   31
FT STRAND    34   39
FT TURN     41   42
FT STRAND    46   51
FT TURN     53   54
FT STRAND    58   60
FT TURN     62   67
FT STRAND    68   73
FT TURN     74   77
FT STRAND    78   83
FT HELIX     88   90
FT STRAND    92   99
FT STRAND   106  106
FT TURN     107  108
FT STRAND   109  109
FT STRAND   113  113
FT STRAND   120  124
SQ SEQUENCE  126 AA;  13718 MW;  14F328CF CRC32;

Query Match          42.4% Score 405; DB 5; Length 126;
Best Local Similarity 45.9%; Pred. No. 4.97e-63;
Matches             61; Conservative 33; Mismatches 31; Indels 8; Gaps
Ddb      1 qvqlve-sgggvgvpgsrslrlscssqgfissyanywvrqpqpkalew--ai-iwdldas 56
            |||||..||..||..||..||..||..||..||..||..||..||..||..||..||..||
QY       1 EVQLLESGAELVPGQSRSLVKASGRFTESCHSVITWVPQAPKQGLPMMRSTPTFGSAN 60
            |||||..||..||..||..||..||..||..||..||..||..||..||..||..||..||
Ddb      57 -dghyvadvkgrftisrdnsknllflqmdslripedtygyfcarogahelcssusctapdy 119
            |||||..||..||..||..||..||..||..||..||..||..||..||..||..||..||
QY       61 YACNVAQWFEPFQNSLIADSTSTSFIELSNLSGULAVYYCANQPPK-YLSAGRGYYGNFF 119
            |||||..||..||..||..||..||..||..||..||..||..||..||..||..||..||
Ddb     116 --wgqgtptvtss 126
            |||||..||||
QY      120 Q-WGGSTILVTYSS 132

RESULT 11
ID HV01_MOUSE STANDARD; PRT: 121 AA.
AC P01745;
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21-JUL-1986 (REL. 01; LAST SEQUENCE UPDATE)
DT 13-AUG-1987 (REL. 05; LAST ANNOTATION UPDATE)
DI IG HEAVY CHAIN V REGION (MPC 11).
DS MUS MUSCULUS (MOUSE).
OS EUKARYOTA; METAZOA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
CC [1]
RP SEQUENCE FROM N.A.
RN MEDLINE; 81053741.
RX ZAKUT F., COHEN J., GIVOL D.:
RL NUCLEIC ACIDS RES. 8:3591-3601(1980).
RC [2]
RP REVISIONS.
RPL ZAKUT R., COHEN J., GIVOL D.:
RPL NUCLEIC ACIDS RES. 8:4839-4840(1980).
CC -:- THIS SEQUENCE WAS TRANSLATED FROM AN mRNA ISOLATED FROM A
CC MYELOMA I-HAL SECRETES 1G32E.
CC PIP: AB2027; GVMS11.
DR HSP; P01810; INFE.
DK IMMUNOGLOBULIN V REGION.
KW NON_TER 121
SQ SEQUENCE 121 AA; 13135 MW; 2AEF08CC CRC32;

Query March 41.2%, Score 394, Eb 5, Length 121;
Best Local Similarity 46.2%, Pred No. 1,27e-60;
Matches 51; Conservative 38; Mismatches 22; Indels 11; Gaps

Db      1 eaql-qgsgaeivrpdtsvskiscagtyftnyiaawkerphalewid---iyppau 54
Qy      1   ||| ||||| :|||:|||||:|||||: |||||: |||||: |||: |
    1 PVGTFEGSGAFVKKPSSVVSKASGRFTESHVITWVEQAPKQGVPMWFSTPIFGSAN 62
Db      57 ft--nyndldkgkalltadssstaviylqsltsedsaiyhbeard---lyvssg--p-yfd 110

```



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RN [1]
RP SEQUENCE.
RX MEDLINE; 80078170.
RA SCHILLING J., CLEVERING B., DAVIE J.M., HOOD L.;
RL NATURE 283:35-40(1980).
CC -1- THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO BIND DEXTRAN
CC DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF WHICH OCCUP IN
CC THE D AND J SEGMENTS.
CC -1- THIS PROTEIN BINDS DEXTRAN
CC PIR; A26242; MHMSJ5.
DR HSP; P01789; 2FGW.
KW IMMUNOGLOBULIN V REGION.
FT DISULFID 22 96 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; E7548A05 CRC32;

Query Match 39.5%; Score 378; DB 5; Length 117;
Best Local Similarity 50.0%; Pred. No. 3,94e-57;
Matches 54; Conservative 29; Mismatches 20; Indels 5; Gaps 3;

Db 1 evql-qsgpelvkpaasvkmsckasgytftdyymkvwkqshkslewlgdinpnnqgts 59
   ||||-|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 1 EVQLLESGAELVRKPSGVSKVCKASGGTFSGHVTWVROAPGGGLEWMGESIPFGSAN 60
   ||||-|||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 60 y--n--qkfkqkatltvdksstaymqlnsltsedsavyyccardrywy 103
   | | ||||:|||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 61 YAQNYAKFRDRVSIIDESTSTSFIELSNLRSDDTAVYYCARDPPRY 108

```

Search completed: Tue Feb 24 07:02:06 1998
 Job time : 23 secs.

WPSRELH (TM)

Release 2.1D John F. Collins, PicoComputing Research Unit.
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MPSrch_pp protein - protein database search, using Smith-Waterman algorithm

Pin on: Tue Feb 24 07:05:52 1998; MasPar time 6.99 Seconds
252.448 Million cell updates/sec

Tabular output not generated.

Title: >US-08-844-215-2
Description: (1-127) from US0844215.pep
Perfect Score: 931
Sequence: 1 EVQLLEQSGAEVKKPGSSVK.....HTMGYFDYWGQGLTVVSS 127

Scoring table: PAM 150
Gap 11

Searched: 111726 seqs, 13889129 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-geneseq30
1:part1 2:part3 3:part4 4:part5 5:part6 6:part7 7:part8
8:part9 9:part10 10:part11 11:part12 12:part13 13:part14
14:part15 15:part16 16:part17 17:part18 18:part19
19:part20 20:part21 21:part22 22:part23 23:part24

Statistics: Mean 30.758; Variance 161.149; scale 0.191

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	616	66.2	147	12	93KA9 anti-Varicella	1.27e-38
2	613	65.8	123	23	CEA-specific antibody	2.20e-38
3	610	65.5	481	5	Sequence of antibody	3.81e-38
4	602	64.7	123	23	CEA-specific antibody	1.65e-37
5	601	64.6	123	23	CEA-specific antibody	1.98e-37
6	600	64.4	123	23	CEA-specific antibody	2.37e-37
7	597	64.1	123	23	CEA-specific antibody	4.10e-37
8	579	62.2	120	9	SPA-reactive IgM heavy	1.10e-35
9	576	61.9	476	6	Antibody D heavy chain	1.90e-35
10	574	61.7	120	9	SPA-reactive IgM heavy	2.74e-35
11	572	61.4	98	12	DR1C VH region	3.94e-35
12	572	61.4	243	14	Humanised 5G1.1 VH +	3.94e-35
13	565	60.7	123	14	HSV-neutralising anti	1.41e-34
14	561	60.3	249	14	Humanised 5G1.1 VH +	2.93e-34
15	558	59.9	119	23	Anti-melanoma antibody	5.06e-34
16	558	59.5	140	23	Humanised heavy chain	5.06e-34
17	554	59.5	248	14	Humanised CDR-grafted	1.05e-33
18	550	59.1	98	12	Humanised VH region	2.17e-33
19	550	59.1	117	4	Human heavy chain V r	2.17e-33
20	550	59.1	117	4	Protein encoded by th	2.17e-33

21	550	59.1	117	20	W03950	DNA fragment vha9.8;	2.17e-33
22	549	59.0	140	23	W21849	Humanised heavy chain	2.61e-33
23	548	58.9	121	14	R77974	Humanised mouse D9G-2	3.13e-33
24	548	58.9	124	9	P45604	Monoclonal antibody G	3.13e-33
25	548	58.9	140	9	P55556	D9G-200 Humanised an	3.13e-33
26	546	58.6	121	16	P88504	VHmu for antibody B13	4.50e-33
27	546	58.6	142	9	P50188	Heavy chain variable	4.50e-33
28	543	58.3	117	2	R41104	Human antibody Eu hea	7.78e-33
29	543	58.3	118	5	R38742	Heavy chain variable	7.78e-33
30	540	58.0	121	5	R25724	Humanised VH region o	1.34e-32
31	540	58.0	140	23	W21850	Humanised heavy chain	1.34e-32
32	535	57.5	142	9	R50194	Heavy chain variable	3.33e-32
33	535	57.5	248	14	R77607	Humanised CDR-grafted	3.33e-32
34	535	57.5	249	14	R77611	Humanised 5G1.1 VH -	3.33e-32
35	535	57.5	468	6	P28804	pre-5A8 humanised hea	3.33e-32
36	531	57.0	124	8	R47931	Mutated humanised hea	5.90e-32
37	531	57.0	140	12	R64265	CDR-grafted L243-gH V	5.90e-32
38	531	57.0	140	12	P42235	Humanized antibody L2	6.90e-32
39	530	56.9	139	11	P62679	CY1748PHB VH region	8.27e-32
40	526	56.5	124	9	R45610	Monoclonal antibody G	1.71e-31
41	526	56.5	139	12	R62578	CY1748PHB VH region	1.71e-31
42	526	56.5	139	8	R43693	PB1.3/Humanised heavy	1.71e-31
43	526	56.5	139	11	P62680	CY1748PHB VH region	1.71e-31
44	526	56.5	139	8	R43689	PB1.3/Humanised heavy	1.71e-31
45	525	56.4	118	4	P22569	Heavy chain VH15.4 fr	2.05e-31

ALIGNMENTS

RESULT 1
ID R65019 standard; Protein; 147 AA.
AC R65019;
DE 02-OCR-1995 (first entry)
DE 93KA9 anti-Varicella zoster virus antibody heavy chain variable.
DE region.
KW Varicella zoster virus; VZW; anti-VZW monoclonal antibody; 93KA9;
KW glycoprotein II subunit; vaccine.
OS Synthetic.
FH Key Location/Qualifiers
FT Protein 20..147
FT /label= mature light chain
FT Region 50..54
FT /label= complementarity determining region (CDR)
FT Region 69..85
FT /label= CDR
FT Region 118..136
FT /label= CDR
FT Region
FN W09504080-A.
PD 09-FEB-1995.
PF 22-JUL-1994; U08241.
PF 28-JUL-1993; US-098479.
PK 24-MAR-1994; US-217918.
PA (SANO) SANDOZ PHARM CORP
PI Lake P, Ostberg L;
DR WPI; 95-090612/12.
DP N-PSDB; 082750.
FT Human monoclonal antibodies specific for the glycoprotein II
FT subunit of varicella zoster virus - used in a therapy and
FT prophylaxis of infection
PS Claim 8; Fig 4B; 39pp; English.
CC A human anti-Varicella zoster virus monoclonal antibody was prep
CC One the tritoma method of Ostberg et al. (1983) Hybridoma 2:361-367.
CC Using resultant tritoma neutralised VZV in the absence of complement.
CC This cell line, designated cell line TC93KA9, produced an antibody
CC designated 93KA9. cDNA for the light and heavy chain variable region
CC genes of the 93KA9 antibody were cloned using PCR. At least two
CC heavy chain (gamma-1) and two light chain (kappa) specific clones
CC were sequenced (see 042749 & 042750 respectively).
SQ Sequence 147 AA:

Query Match 66.2%; Score 115; DB 12; Length 147;
Best Local Similarity 66.7%; Prod No. 1.27e-38;
Matches 86; Conservative 19; Mismatches 12; Indels 2; Gaps 0;

Db	60	yaqkfqgrllitadeststajmolelsrddlatvyyccarhahcyel-yy--ymdswaqa	115
QY	61	YAKRFQGSLLACDSTATYAMELSPSECTAVYFCAPVVPKAPHTMYFFIYFWGQ	120
Db	117	tmvtvss	123
QY	121	TLVTVSS	127

RESULT	3
ID	P24442 standard; Protein; 481 AA.
AC	P24442.
DI	Q2-JAN-1932 (first entry)
DE	Sequence of antibody molecule IgG1.
KW	Antibody; immunoglobulin G1.
OS	Homo sapiens.
PH	Key
	Location/Qualifiers

91. CONSERVATIVE 14. MISMAJES 21. INDEN 27. GUP
 25. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840. 841. 842. 843. 844. 845. 846. 847. 848. 8

DE CEA-specific antibody CEA6 VH sequence.
 KW Carcinoembryonic antigen; CEA; human; antibody; scFv;
 KW tumour marker; lung cancer; breast cancer; colon cancer;
 KW adenocarcinoma; diagnosis.

OS Homo sapiens.

FT Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1

FT /note= "complementarity determining region 1"

FT Region 50..66

FT /label= CDR2

FT /note= "complementarity determining region 2"

FT Region 99..112

FT /label= CDR3

FT /note= "complementarity determining region 3"

FT Region 12..JUN-1997.

PD 09-DEC-1996; G03043.

PR 11-OCT-1996; GR-021295.

PR 07-DEC-1995; GR-025004.

PR 23-MAY-1996; GR-010824.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Allen DJ, McCafferty JG, Osbourn JK;

DR WPI: 97-319779/29.

DR N-PSDB: T72131.

PT Specific binding members for human carcinoembryonic antigen - bind
 to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells; used for diagnosing
 PT cancer

PS Claim 4; Fig 1a; 128pp; English.

CC This polypeptide sequence comprises the heavy chain variable
 CC region (VH) of human carcinoembryonic antigen (hCEA)-specific
 CC antibody CEA6. VH (T72133-35) and VL (T72133-35) gene sequences
 CC were obtained for anti-hCEA antibodies CEA1-CEA7 (see W19876-85).
 CC A claimed specific binding member (A) comprises an hCEA specific
 CC antibody antigen binding domain that has a dissociation constant
 CC for hCEA of less than 1×10^{-8} M, is non-cross-reactive with human
 CC liver cells, and preferentially binds to the A3-B3 extracellular
 CC domain of hCEA and/or to cell-associated hCEA over hCEA over
 CC soluble hCEA. Preferred (A) include pairings of VH and VL
 CC sequences from CEA1-7, or their CDR sequences, as well as CEA6
 CC VH and VL variants, including combinations of CEA6 VH with VL
 CC regions from CEA6, T06D4, T06D6, L06D12, L06D17 or L06D2.
 CC (A) is used to detect cells expressing hCEA, in vivo or in vitro,
 CC especially tumour cells for diagnosing cancer, e.g. adenocarcinoma
 CC of the colon, lung or breast.

CC Sequence 123 AA;

Query Match 64.4%, Score 600; DB 23, Length 123;
 Best Local Similarity 71.7%; Pred. No. 2.37e-37;
 Matches 91, Conservative 10; Mismatches 22, Indels 4, Gaps 3,

Db 1 qvqlv-qsgaevkpkssvkvsckaggtfnsqinwlrqapqqlqwmmsliptstlan 59

QY 1 EVQLLESGAEEVKKPKSSVKVSCKAGGTFSYIQLWLRQAPQQLQWMMSLIPTNTEN 60

Db 60 yaqkfqrlltadeststymelsslrscdtavyyca q tascstststyyymdrqqq 116

QY 61 YAQKFQGPLSTADDSSTAYMEISSLRSEDTAVYFAPVVPINAPHTMGYYFDWYGQ 120

Db 117 tmvtvss 123

QY 121 TLVTVSS 127

RESULT 7

ID W19887 standard; Protein, 123 AA.

AC W19887;

DE CEA-specific antibody CEA6 VH mutant HBA11 sequence.

KW Carcinoembryonic antigen; CEA; human; antibody; scFv;

KW tumour marker; lung cancer; breast cancer; colon cancer;

KW adenocarcinoma; diagnosis.

OS Chimeric Homo sapiens;

OS Chimeric synthetic.

FT Key Location/Qualifiers

FT Region 31..35

FT /label= CDR1

FT /note= "complementarity determining region 1"

FT Region 50..66

FT /label= CDR2

FT /note= "complementarity determining region 2"

FT Region 99..112

FT /label= CDR3

FT /note= "complementarity determining region 3"

FT W09720932-A1.

PD 12-JUN-1997.

PD 09-DEC-1996; G03043.

PR 11-OCT-1996; GR-021295.

PR 07-DEC-1995; GR-025004.

PR 23-MAY-1996; GR-010824.

PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Allen DJ, McCafferty JG, Osbourn JK;

DR WPI: 97-319779/29.

PT Specific binding members for human carcinoembryonic antigen - bind
 to the A3-B3 extracellular domain of hCEA and are substantially
 PT non-cross-reactive with human liver cells; used for diagnosing
 PT cancer

PS Claim 4; Fig 2; 128pp; English.

CC This polypeptide sequence comprises the heavy chain variable region
 CC (VH), HBA11, obtained by mutagenesis of the VH CDR3 of human
 CC carcinoembryonic antigen (hCEA)-specific antibody CEA6 (see
 CC W19881). A claimed specific binding member (A) comprises an hCEA
 CC specific antibody antigen binding domain that has a dissociation
 CC constant for hCEA of less than 1×10^{-8} M, is non-cross-reactive
 CC with human liver cells, and preferentially binds to the A3-B3
 CC extracellular domain of hCEA and/or to cell-associated hCEA over
 CC hCEA over soluble hCEA. Preferred (A) include pairings of VH and
 CC VL sequences from CEA1-7 (see W19876-85), or their CDR sequences,
 CC as well as CEA6 VH and VL variants (see W19886-95) obtained by
 CC mutagenesis or chain shuffling (A) is used to detect cells
 CC expressing hCEA, in vivo or in vitro, especially tumour cells for
 CC diagnosing cancer, e.g. adenocarcinoma of the colon, lung or breast.

CC Sequence 123 AA;

Query Match 64.1%, Score 607; DB 24, Length 124;
 Best Local Similarity 71.7%; Pred. No. 4.10e-37;
 Matches 91; Conservative 14; Mismatches 18; Indels 4; Gaps 3;

Db 1 qvqlv-qsgaevkpkssvkvsckaggtfnsqinwlrqapqqlqwmmsliptstlan 59

QY 1 EVQLLESGAEEVKKPKSSVKVSCKAGGTFSYIQLWLRQAPQQLQWMMSLIPTNTEN 60

Db 60 yaqkfqrlltadeststymelsslrscdtavyyca q tascstststyyymdrqqq 116

QY 61 YAQKFQGPLSTADDSSTAYMEISSLRSEDTAVYFAPVVPINAPHTMGYYFDWYGQ 120

Db 117 tmvtvss 123

QY 121 TLVTVSS 127

RESULT 8

ID R54796 standard; peptide; 120 AA.

AC R54796;

DE 18-OCT-1994 (first entry)

KW SPA-reactive IgM heavy chain clone KAS.

KW SPA domain D; Ig binding region; IgM; R-cell supernatant; scFv;

KW superantigen, heavy chain variable region; VH3 restricted antibody;

KW VE, protein-A, KAS, B-lymphocyte, vaccine.

OS Homo sapiens.

PN W09409818-A.

PD 11-MAY-1994.

PR 29-OCT-1993; U10555.

PR 30-OCT-1992; US-960936.

PA (REGC) UNIV CALIFORNIA.

PI Silverman GJ;
 DR WPI: 94-167127/20.
 PT Stimulating prodn. of variable region gene family restricted
 PS Antibodies - through B-cell super-antigen vaccination
 CC A B-cell superantigen (sAg) is a fragment of SpA D domain that
 CC specifically binds the Fab portion of variable region of VH, especially
 CC antibodies. The sAg is used to enhance production of VH, especially
 CC VH3, restricted Abs. During attempts to identify sAg, aa sequences
 CC (R54784-801) of H chains from Ig reactive with mod-SpA, and aa and
 CC DNA sequences (P54802-16, Q54842-56) of VH regions of SpA binders
 CC obtained from combinatorial libraries were determined. IgM protein
 CC KAS is derived from the germline configuration of a VH gene
 CC segment.
 SQ Sequence 120 AA;
 Query Match 62.2%; Score 579; DB 9; Length 120;
 Best Local Similarity 67.5%; Pred. No. 1.10e-35;
 Matches 85; Conservative 17; Mismatches 18; Indels 6; Gaps 3;
 Db 1 vhlv-qsgaevkpkpssvkvscasgggtfssvsaivswrqpqgglwmggiipfgqany 59
 QY 2 VQLLESGAEVKKPSSVKVSCQVGFDSRYTIQWLQAPQCGPEWMGNIIPTNTPNY 61
 Db 60 aqfgrvritadestntaymelrlrsddtamycakegydydr-p-----fdwgggt 114
 QY 52 AKKPKELSLIALTCSIAVMELSLSPSTAVYFCAPVVFNAIPHTWGYVFEWVGJST 121
 Db 115 lvtvss 120
 QY 122 LVTVSS 127
 RESULT 9
 ID F31022 standard; Protein; 476 AA.
 AC R31023;
 DT 19-MAY-1993 (first entry)
 DE Antibody D heavy chain.
 KW Heavy, light, chain; antibody; D: monoclonal; peripheral; blood;
 KW lymphocyte; hepatitis A virus; HAV; sero: positive; patient;
 KW murine; B583; polyadenylated; cDNA library; human; kappa; L; H.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /note= "Signal peptide"
 FT Region 20..49
 FT /label= FR1
 FT Region 50..54
 FT /label= CDR1
 FT Region 55..68
 FT /label= FR2
 FT Region 69..84
 FT /label= CDR2
 FT Region 85..113
 FT /label= FR3
 FT Region 114..121
 FT /label= CDR3
 FT Region 122..132
 FT /label= FR4
 FT Domain 133..241
 FT /label= CH1
 FT Region 242..262
 FT /label= HINGE
 FT Domain 263..379
 FT /label= CH2
 FT Domain 380..497
 FT /label= CH3
 PN EP-523949-A.
 PD 20-JAN-1993.
 PF 14-JUL-1992; 306420.
 PR 15-JUL-1991; GB-015284.
 PR 01-AUG-1991; GB-016594.
 PR 23-MAY-1992; GB-006294.
 PA (WELL) WELLCOME FOUND LTD.
 PI Crowe JS, Lewis AP;
 DR WPI: 93-019951/03.
 DR N-PSDB: Q35099.
 PT Prodn. of recombinant primate antibodies - useful for treating
 PT infections caused by hepatitis A, B and C, herpes,
 PT cytomegalovirus, AIDS, APC, also treat multiple sclerosis,
 PT arthritis etc.
 PS Disclosure; Fig 2: 35pp; English.
 CC The sequences given in R31023-24 represent the heavy and light chains
 CC of Antibody D respectively. Antibody D is a monoclonal antibody which
 CC was derived from peripheral blood lymphocytes from a hepatitis A virus
 CC (HAV) sero positive patient. Antibody D is closely related in nature
 CC to murine antibody B5B3. Total RNA was isolated from antibody D
 CC expressing cells and polyadenylated RNA was extracted. These polyA
 CC RNA's were used to prepare a cDNA library which was screened for human
 CC kappa light (L) chains and two positive clones were detected.
 CC Further heavy (H) chain clones were also isolated.
 SQ Sequence 476 AA;
 Query Match 61.9%; Score 576; DB 6; Length 476;
 Best Local Similarity 67.4%; Pred. No. 1.90e-35;
 Matches 87; Conservative 15; Mismatches 22; Indels 4; Gaps 3;
 Db 20 qmgv-qsgaevkpkpssvkvscasgggtfssvsaivswrqpqgglwmggiipfgtpt 78
 QY 1 EVVLLESGAEVKKPSSVKVSCQVGFDSRYTIQWLQAPQCGPEWMGNIIPTNTPN 60
 Db 79 ysqnfgvritadkstahmelrlrsddtamycatdryrqanfdrrvgw-fdpwg 137
 QY 61 YAQKFCRLSITADSTSTAYMELSLSPSEDATAYVPCA--PVVIPAIPHTWGYVFDYWG 118
 Db 138 qgtlvvss 146
 QY 119 QGILVIVSS 127
 RESULT 10
 ID R54795 standard; peptide; 120 AA.
 AC R54795;
 DT 18-OCT-1994 (first entry)
 DE SPA-reactive IgM heavy chain clone BOR.
 KW SPA domain D; Ig binding region; IgM; B-cell superantigen; sAg;
 KW superantigen; heavy chain variable region; VH3 restricted antibody;
 KW VH: protein-A; BOR; B-lymphocyte; vaccine.
 OS Homo sapiens.
 PN WQ9409818-A.
 PD 11-MAY-1994.
 PF 29-OCT-1993; U10555.
 PF 30-OCT-1992; US-969936.
 PA (PEGC) UNIV CALIFORNIA.
 PI Silverman GJ;
 DR WPI: 94-167127/20.
 PT Stimulating prodn. of variable region gene family restricted
 PT antibodies - through B-cell super-antigen vaccination
 PS Disclosure; Page 77; 130pp; English.
 CC A B-cell superantigen (sAg) is a fragment of SpA D domain that
 CC specifically binds the Fab portion of variable region of VH, especially
 CC antibodies. The sAg is used to enhance production of VH, especially
 CC VH3, restricted Abs. During attempts to identify sAg, aa sequences
 CC (R54784-801) of H chains from Ig reactive with mod-SpA, and aa and
 CC DNA sequences (R54802-16, Q54842-56) of VH regions of SpA binders
 CC obtained from combinatorial libraries were determined. IgM protein
 CC BOR is derived from the germline configuration of a VH gene
 CC segment.
 SQ Sequence 120 AA;
 Query Match 61.7%; Score 574; DB 9; Length 120;
 Best Local Similarity 69.8%; Pred. No. 2.74e-35;
 Matches 88; Conservative 15; Mismatches 17; Indels 6; Gaps 3;
 Db 1 vqlv-qsgaevkpkpssvkvscasgggtfssvsaivswrqpqgglwmggiipfgtpt 59
 QY 2 VQLLESGAEVKKPSSVKVSCQVGFDSRYTIQWLQAPQCGPEWMGNIIPTNTPNY 61

```

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FT Region
FT /label CEF-H2
FT Region          118 130
FT /label= CDR-H3
FT Region
PN WQ9529697-A1..
PD 09-NOV-1995.
PF
PR Q1-MAY-1995; 005688.
PR Q2-MAY-1994; US-235208.
PA (ALEX-) ALEXION PHARM INC.
PI Evans M., Mattis L., Mueller EE., Nye SH., Roilivas S.;
PI Rother RP., Springhorn J P., Squitton SP., Thomas TC.;
PI Wang Y., Wilkins JA.;
PI WPI: 95-292923/50.
DP
DR N:PDB; T08483..
PT Treating glomerulonephritis with antibody against complement C5
PT component - to inhibit complement induced cell lysis
PI Example 11, Page 119-122, 181pp, English.
FS A humanised CDK-grafted and framework sequence-altered Fd, 5G1.1 VH
CC + IGHL (P77610). It includes CDRs derived from mouse anti-C5 monoclonal
CC antibody 5G1.1. It can be co-expressed with a humanised light
CC chain (J77612) in human 29A RNA cells using encoding DNAs
CC subcloned into vector APEX-AP (T08476). Such humanised recombinant
CC antibodies retain the ability of Mab 5G1.1 to block human complement
CC C5a generation and thus to reduce glomerular inflammation and kidney
CC dysfunction associated with glomerulonephritis.
CC Sequence 249 AA;
SQ

Query Match:           51.4%; Score 572; DR 14; Length 249;
Best Local Similarity 68.5%; Pred.No. 3,94e-35;
Matches 87; Conservative 16; Mismatches 19; Indels 5; Gaps

Db    20 qvqlv-qsgaevkkgqgskvkscksgyifsnwlaqvrggqggglewmgailpkasiste 78
      ::::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY    1 EVALLDSAEVKKKPKSSSVKVSCTGVESITFSPYTIGLRGPAGQGPEWGNIIIVYNIPN 60

Db    79 yackfggrvtmdtstststaymelslrdsotavyygcaryffacs-pn---wyfdvwdaq 134
      |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
QY    51 YAKFKPSPLSTAGLSTSTAYMELSLSPSELTAVYFAKVVIENAIHRIIMGYVYFDVWQGL 120

Db    135 tlrvss 141
QY    121 tlvrvss 127

RESULT 13
ID   P76964 standard; peptide: 122 AA.
DC   R76964;
DT   22-FEB-1996. (first entry)
DE   HSV-neutralising antibody clone FabHSV8 heavy chain.
KW   herpes simplex virus, type 1, type II, monoclonal antibody;
KW   diagnosis; neutralisation; immunotherapy.
OS   Homo sapiens.
PN   W09518634-A1..
PD   13-JUL-1995.
PR   Q4-JAN-1995; 000067.
PR   Q4-JAN-1994; US-178201.
PA (SCRI ) SCRIPPS PES INST.
PA Burioni R., Burton DE., Sanna PP., Williamson RA.;
PP WPI: 95-254909/33.
PT Human monoclonal antibodies that neutralise Herpes simplex virus
PT (HSV) types 1 and 2 - used for diagnosis and passive immunotherapy
PT of HSV infections.
PS Disclosure; Page 72; 100pp; English.
FS P76964 is the heavy chain of the human anti-herpes monoclonal antibody
CC clone FabHSV8. This antibody is capable of neutralising both herpes
CC simplex virus (HSV) types I and II by binding an epitope present on
CC glycoprotein D. The antibody may be used for detecting HSV in vitro or
CC in vitro; for passive immunotherapy (pref. prophylactically) of HSV
CC infection (eg. genital, oral or ocular herpes), partic. as its Fab
CC fragment and as a competitive reagent for detecting neutralising
CC anti-HSV antibodies in a sample. Anti-idiotypic antibodies raised
CC against the mAb can be used for active immunotherapy of HSV infection

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SQ Sequence 122 AA:

Query Match 60.7%; Score 565; DB 14; Length 122;
 Best Local Similarity 66.7%; Pred. No. 1.41e-34;
 Matches 92; Conservative 14; Mismatches 26; Indels 1; Gaps 1;

Db 1 leqsaevkkgssvkvsckasgssfsyalnwrqpgqglwmgglpifgtanyakg 60
 QY 5 LEQSAEVKKGSSVKVSCQVFGDTFSYTIQWLPQAPGQGPWGMNIPVYNTPNYAKK 64
 Db 61 fgdrlitadvststamqlsglyedtamycarvaymlpvttagg-ldwzgggtvt 119
 QY 65 FGDRLITADVSTSTAMVWELSSLSSEDAVVFCAVVPNAIRHTMGVYFDYWGQGLT 124
 Db 120 *as 122
 QY 125 VSS 127

RESULT 14

ID R77615 standard; Protein: 249 AA.

AC R77615:

DT 02-APR-1996 (first entry)

DE Humanised 5G1.1 VH + IGHRLD.

KW Complement C5; haemolysis; kidney; glomerulonephritis;

KW monoclonal antibody; antiinflammatory; antibody engineering;

KW humanised antibody; complementarity determining region; CDR.

OS Synthetic.

FH Key Location/Qualifiers

FT Peptide 1 19

FT /label= sig_peptide

FT Peptide 20..249

FT /label= mat_peptide

PN W09529697-A1.

PD 09-NOV-1995.

PF 01-MAY-1995; U05688.

PR 02-MAY-1994; US-236208.

PA (ALEX-) ALEXION PHARM INC

PI Evans MJ, Matis L, Mueller EE, Nye SH, Rollins S;

PI Rother RP, Springhorn J P, Squinto SP, Thomas TC;

PI Wang Y, Wilkins JA;

DR WPI: 95-392923/50.

DR N-ESDB: T08487.

PT Treating glomerulonephritis with antibody against complement C5

PT component - to inhibit complement induced cell lysis

PS Claim 37: Pages 135-137; 181pp; English.

CC A DNA construct (T08487) codes for a humanised CDR-grafted

CC light chain, designated 5G1.1 VL + IGHRLD (R77615), which includes

CC CDRs derived from mouse anti-C5 monoclonal antibody 5G1.1. The

CC DNA can be subcloned together with DNA (T08484) coding

CC for a humanised Fd (R77611) into vector APEX-3P (T08476) for

CC expression of humanised antibody in human 293 EBNA cells. Such

CC recombinant antibodies retain the ability of Mab 5G1.1 to block

CC human complement C5a generation and thus to reduce glomerular

CC inflammation and kidney dysfunction associated with

CC glomerulonephritis.

SQ Sequence 249 AA:

Query Match

Best Local Similarity 66.9%; Score 561; DB 14; Length 249;

Matches 85; Conservative 16; Mismatches 21; Indels 5; Gaps 3;

Db 20 qvqlv-qsgaevkkgssvkvsckasgssfsyalnwrqpgqglwmgglpifgtanyakg 78
 QY 1 EVQQLVQSGAEGVKKVKGSSVKVSCQVFGDTFSYTIQWLPQAPGQGPWGMNIPVYNTPN 60

Db 79 yaqfqrvttrtdststymelsslsrsdctavyycar-pn---wyfdwvqgg 134
 QY 61 YAQFQRVLTTRDSTSTAYMELSSLSRSDCTAVYVFCARVVPNAIRHTMGVYFDYWGQ 120

Db 135 tlvtvss 141

QY 121 TLTVSS 127

RESULT 15

ID W13536 standard; protein; 119 AA.

AC W13536;

DT 28-OCT-1997 (first entry)

DE Anti-melanoma antibody; 2-71 from VH antibody; fusion phage library.

KW Human; monoclonal antitumour antibody; peripheral blood lymphocyte;

KW cancer; tumorigenesis; anticancer vaccine.

OS Homo sapiens.

PN W09702479-A2.

PD 23-JAN-1997.

PE 28-JUN-1996; IB1032.

PR 30-JUN-1995; US-497647.

PA (OYYA) UNIV YALE.

PI Cai X, Garen A;

DR WPI: 97-109061/10.

PT Prodn. of human monoclonal anti-tumour antibodies - by screening a

PT fusion phage library produced using peripheral blood lymphocytes

PT from a cancer patient

PS Claim 19; Page 75-76; 82pp; English.

CC A process for isolating and synthesising human monoclonal anti-tumour

CC antibodies has been produced. The process involves: (a) constructing at

CC least one fusion phage library from the peripheral blood lymphocytes

CC (PBUs) of a cancer patient; (b) screening for anti-tumour antibodies in

CC the phage library in a binding assay with cultured tumour cells of the

CC same type as the patient's tumour; (c) removing extraneous antibodies by

CC absorption against normal human cells; (d) cloning the phage selected in

CC step (b) and (c); (e) assaying the specificity of the cloned phage by

CC incubating the phage with at least two types of cultured normal cells;

CC and (f) further testing the specificity of cloned phage that do not bind

CC to either cell line of cultured normal cells in further binding assays

CC to cultured tumour cells derived from more than one other tumour that is

CC not the patient's tumour. The present sequence represents a human heavy

CC chain antibody, from a VH antibody fusion phage library, produced by

CC a method as described above. The antibodies produced can be used for

CC diagnostic and therapeutic applications and for isolating tumour

CC antigens for studying tumourigenesis or for use as anti-cancer vaccines.

CC The human antibodies have low immunogenicity in humans compared to

CC murine monoclonal antibodies (MABs). Since the antibodies are isolated

CC from fusion phage libraries, their affinity and specificity for a

CC tumour cell line can be improved by genetic manipulations.

SQ Sequence 119 AA:

Query Match 59.9%; Score 558; DB 23; Length 119;

Best Local Similarity 71.7%; Pred. No. 5.06e-34;

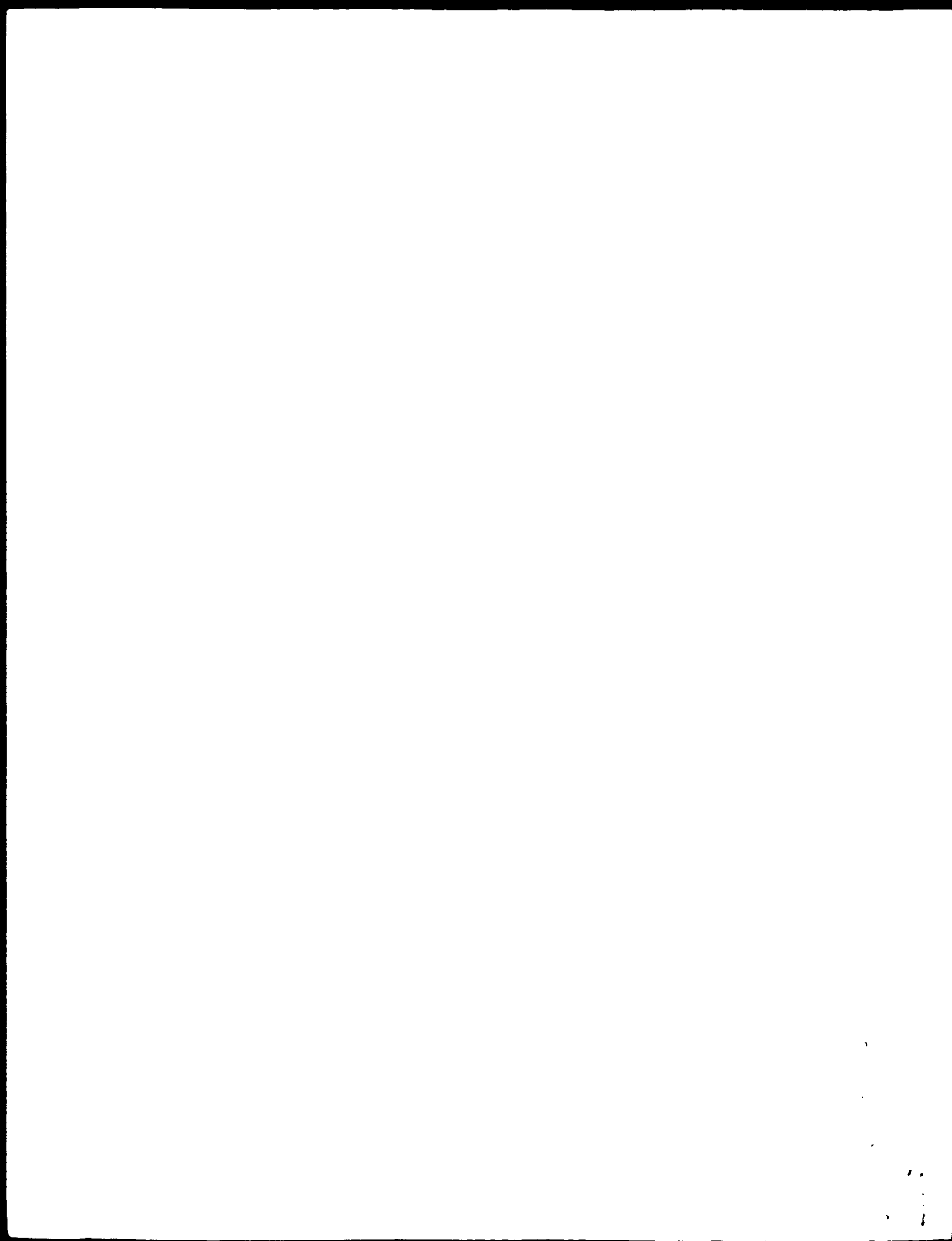
Matches 86; Conservative 11; Mismatches 16; Indels 7; Gaps 4;

Db 7 gglevkkpgssvkvsckasggtfssyalnwrqpgqglwmgglpifgtanyakfgg 66
 QY 8 SGAEVKKPGSSVKVSCQVFGDTFSYTIQWLPQAPGQGPWGMNIPVYNTPNYAKFGG 67

Db 67 rvtitadkdststamylsslsrsdctavyycar---ggg-ryd-a--fdwvqgglvtvss 119
 QY 68 RVTITADKSTSTAYMELSSLSRSDCTAVYVFCARVVPNAIRHTMGVYFDYWGQGLTVTSS 127

Search completed: Tue Feb 24 07:06:25 1998

Job time : 33 secs.



RESULT

SOURCE

DEFINITION

A0377074 291 bp mpNA EST 21-APR-1997
EST8603 Small Intestine Homo sapiens cDNA 5' end similar to
sequence encoding aminoacyl-tRNA heavy chain, VHS regions (AF024165).

A0377074
A0377074 NID KEYWORDS EST SOURCE:
human.

Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, J.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudok, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.K., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Forrie, A., Fischer, C., Hastings, G.A., He, W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olson, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Pannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
96026280

COMMENT

Contact: Kerlavage, AR
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The Institute for Genomic Research
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Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tgr/hgi/hgi.html>)
Seq primer: M13 Reverse

FEATURES

source
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ORIGIN

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Matches 81; Conservative 0; Mismatches 45; Indels 0; Gaps 0;
Db 121 gaggtgagttgtggaatctgaggaagcctggtacagaccgggggtctcctgaagctc 180
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QY 1 GAGGTGAGCTGCTCGACTGTGACTGTGAGGTGAGGTGAGGTGAGGTGAGGTGAG 60
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Db 181 tctgtgagcctctggaattcttcaacagttacagatgaactgggtcgcagctc 240
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 TCCTGCAGGCGCTCGAGGAGCTTCAGAGCTACAAATTTCAATGGGTGCGACAGGCTC 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 caggga 246
QY 121 CCTGGA 126

RESULT 14
LOCUS AA378312 366 bp mRNA EST 21-APR-1997
DEFINITION EST91017 Synovial sarcoma Homo sapiens cDNA 5' end similar to similar to immunoglobulin gamma 1 heavy chain, C region
ACCESSION AA378312
NID 92030651
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
1 (bases 1 to 366)
AUTHORS Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Feldner, R.A., Bult, C.J., Lee, N.H., Kirkness, F.F., Weinstock, P.C., Garyay, J.D., White, O., Sutton, G., Blake, J.A., Brandon, P.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geodhagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Li, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, J.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudok, D.M., Shirley, R.,

Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geodhagen, N.S., Glodek, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Li, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palancas, R.F., McDonald, J.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudok, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.K., Weidman, J.F., Li, Y., Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dimke, D., Feng, D.-F., Forrie, A., Fischer, C., Hastings, G.A., He, W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olson, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Pannon, M.P., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M., and Venter, J.C.
Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl.), 3-174 (1995)
96026280

COMMENT

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9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tgr/hgi/hgi.html>)
Seq primer: M13 Reverse

FEATURES

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/dev_stage="adult, 20 yrs"
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BASE COUNT
ORIGIN

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Matches 40; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 24 taagcagctgagacccagagacagcagcagcagcagcagcagcagcagcagcagcagc 68
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QY 24R TAGAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 292
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
LOCUS AA381086 278 bp mRNA EST 21-APR-1997
DEFINITION EST94138 Activated T-cells XII Homo sapiens cDNA 5' end similar to similar to immunoglobulin mu heavy chain, V region.
ACCESSION AA381086
NID 92033426
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryotae; mitochondrial eukaryotes; Metazoa; Chordata;
Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea;
Homo.
1 (bases 1 to 278)

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